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NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48		
NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59		
NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	**	-
NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2		
NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37		
NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	**	+
NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69		
NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57		
NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85		
NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18		
NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85		
NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	*	-
NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31		
NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	*	-
NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54		
NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06		
NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27		
NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52		
NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65		
NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74		
NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21		
NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06		
NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9		
NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16		
NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	*	+
NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97		
NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	**	+
NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77		
NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	*	+

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NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85		
NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		
NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+
NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-



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NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		
NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		
NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8		
NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19		
NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66		
NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*	+
NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21		

NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63		
NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*	-
NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*	+
NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*	+
NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53		
NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91		
NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3		
NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06		
NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93		
NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24		
NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07		
NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*	-
NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*	-
NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64		
NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33		
NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29		
NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49		
NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37		
NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12		
NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13		
NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51		
NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96		
NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79		
NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54		
NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59		
NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01		
NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*	+
NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94		
NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69		

NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57
NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06
NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42
NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72
NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06
NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16
NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04
NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39
NT2RP3003076	2.67	2.67	9.49	6.57	6.57	4.01
NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43
NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97
NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25
NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93
NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73
NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18
NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91
NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44
NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96
NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29
NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74
NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7
NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72
NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97
NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94
NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62
NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65
NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2
NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27
NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79

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NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66		
NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36		
NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44		
NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64		
NT2RP3003226	3.25	3.25	5.68	6.57	5.94	3.63		
NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72		
NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89		
NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25		
NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08		
NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42		
NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47	**	+
NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68		
NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86		
NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72		
NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63		
NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19		
NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	**	-
NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	*	-
NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23		
NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91		
NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	**	+
NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41		
NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87		
NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34		
NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	**	+
NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6		
NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24		
NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	**	+
NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45		

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NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5		
NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63		
NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62		
NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65		
NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	**	-
NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	*	-
NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32		
NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92		
NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03		
NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96		
NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85		
NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49		
NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45		
NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03		
NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87		
NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77		
NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63		
NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44		
NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08		
NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2		
NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07		
NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	**	+
NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52		
NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28		
NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12		
NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26		
NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45		
NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65		
NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72		

NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13
NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19
NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97
NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83
NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55
NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58
NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23
NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49
NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25
NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32
NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22
NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75
NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58
NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74
NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49
NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09
NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96
NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96
NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71
NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4
NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83
NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53
NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13
NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04
NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09
NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3
NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88
NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64
NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55

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NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96		
NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29		
NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	*	+
NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12		
NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88		
NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88		
NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25		
NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27		
NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74		
NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57		
NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96		
NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14		
NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24		
NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18		
NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45		
NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32		
NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6		
NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45		
NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94		
NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59		
NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73		
NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81		
NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43		
NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06		
NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*	-
NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97		
NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27		
NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52		
NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76		

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NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37		
NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	*	+
NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24		
NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75		
NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91		
NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89		
NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82		
NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35		
NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	*	+
NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75		
NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55		
NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23		
NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96		
NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31		
NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09		
NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2		
NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32		
NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05		
NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68		
NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88		
NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	**	-
NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	*	+
NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81		
NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73		
NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53		
NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37		
NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39		
NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6		
NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42		



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NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96		
NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91		
NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85		
NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09		
NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06		
NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88		
NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49		
NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52		
NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	**	+
NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48		
NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96		
NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84		
NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92		
NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61		
NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05		
NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8		
NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62		
NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11		
NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84		
NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57		
NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88		
NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01		
NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	*	+
NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81		
NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67		
NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22		
NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69		
NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78		
NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17		

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NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47		
NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11		
NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33		
NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47		
NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47		
NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3		
NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79		
NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37		
NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32		
NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03		
NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	**	+
NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47		
NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55		
NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21		
NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97		
NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73		
NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38		
NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08		
NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05		
NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81		
NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59		
NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5		
NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59		
NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18		
NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-
NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-
NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7		
NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28		
NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26		

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NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+
NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3		
NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28		
NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9		
NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-
NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+
NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55		
NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65		
NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56		
NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8		
NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8		
NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39		
NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-
NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-
NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57		
NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99		
NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+
NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83		
NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31		
NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34		
NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56		
NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72		
NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06		
NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63		
NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47		
NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13		
NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48		
NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54		
NT2RP3004349	5	5	7.5	4.89	7.75	5.76		

NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18		
NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56		
NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85		
NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+
NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75		
NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+
NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06		
NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93		
NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12		
NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51		
NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83		
NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09		
NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38		
NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99		
NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63		
NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48		
NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5		
NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61		
NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72		
NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88		
NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9		
NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82		
NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39		
NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25		
NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08		
NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92		
NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88		
NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52		
NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82		

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NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68		
NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75		
NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62		
NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*	-
NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38		
NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12		
NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25		
NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48		
NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98		
NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98		
NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	*	+
NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1		
NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79		
NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91		
NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07		
NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24		
NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29		
NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28		
NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94		
NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27		
NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34		
NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39		
NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9		
NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1		
NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47		
NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32		
NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12		
NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	*	+
NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34		

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NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46		
NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23		
NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77		
NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87		
NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98		
NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	*	+
NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01		
NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68		
NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3		
NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05		
NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96		
NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		

NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		

NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+
NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92		
NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75		
NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12		
NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08		
NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24		
NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38		
NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2		
NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48		
NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04		
NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13		
NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73		
NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83		
NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99		
NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95		
NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5		
NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59		
NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03		
NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02		
NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79		
NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61		
NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08		
NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13		
NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12		
NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68		



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NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19		
NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46		
NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27		
NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48		
NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27		
NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67		
NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12	**	+
NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4		
NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58		
NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98		
NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6		
NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37		
NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36		
NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98		
NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66	**	-
NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35	*	+
NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66		
NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33		
NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26		
NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91		
NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65		
NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9	*	+
NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49		
NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39	*	-
NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51	*	+
NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12		
NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82		
NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79		
NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82		

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NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77		
NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3	**	-
NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01		
NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52		
NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09	*	+
NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75		
NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78		
NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03		
NT2RP4000549	23.81	23.81	56.48	41.6	51.57	38.82		
NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07		
NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27		
NT2RP4000558	30.12	30.12	94.28	68.16	57.01	73.2		
NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12		
NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46	*	+
NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56		
NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24		
NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55	*	+
NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65		
NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59		
NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12		
NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35		
NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19		
NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31		
NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73		
NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19		
NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49		
NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73		
NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12		
NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14		

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NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71		
NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52		
NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83		
NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33	**	-
NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83		
NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28		
NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84		
NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68		
NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2		
NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27		
NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55		
NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67		
NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54	*	-
NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73		
NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45		
NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62		
NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82		
NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22		
NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6		
NT2RP4000823	697.74	697.74	1127.48	923.16	1026.8	947.85		
NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69		
NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91		
NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		
NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		

NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+
NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		

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NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+
NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		
NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		

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NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+

NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		
NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97		
NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74		
NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24		
NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89		
NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11		
NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76		
NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06		
NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62		
NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87		
NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42		
NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86		
NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08		
NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16		
NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07		
NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48		
NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94		
NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38		
NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27		
NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32		

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NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09		
NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*	-
NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76		
NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84		
NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8		
NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8		
NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41		
NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38		
NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	*	+
NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	*	-
NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41		
NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57		
NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8		
NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97		
NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98		
NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19		
NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42		
NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91		
NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13		
NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83		
NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37		
NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	**	+
NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02		
NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	*	-
NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05		
NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19		
NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98		
NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29		
NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81		



NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45		
NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81		
NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02		
NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74		
NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68		
NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97		
NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18		
NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13		
NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29		
NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24		
NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92		
NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68		
NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04		
NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66		
NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75		
NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78		
NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7		
NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86		
NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02		
NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	**	+
NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26		
NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	**	-
NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99		
NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21		
NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07		
NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02		
NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31		
NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53		
NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78		

NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87		
NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72		
NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42		
NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15		
NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28		
NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43		
NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98		
NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3		
NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98		
NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97		
NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64		
NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96		
NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22		
NT2RP4001790	2	2	5.29	3.42	2.97	2.58		
NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34		
NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67		
NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95		
NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33		
NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71		
NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33		
NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24		
NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	*	+
NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3		
NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78		
NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71		
NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46		
NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58		
NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39		
NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	*	+

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NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73		
NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91		
NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72		
NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92		
NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15		
NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69		
NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93		
NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12		
NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52		
NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82		
NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89		
NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22		
NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55		
NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71		
NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77		
NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66		
NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16		
NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	*	-
NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36		
NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52		
NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88		
NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02		
NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	*	+
NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42		
NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	**	+
NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36		
NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54		
NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5		
NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11		

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NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	*	+
NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37		
NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75		
NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41		
NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22		
NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	*	-
NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27		
NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27		
NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97		
NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42		
NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88		
NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51		
NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55		
NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72		
NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22		
NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65		
NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	**	+
NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42		
NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21		
NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69		
NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88		
NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19		
NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58		
NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78		
NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17		
NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41		
NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78		
NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29		
NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98		

NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16
NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19
NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13
NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56
NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75
NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68
NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08

NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58		
NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3		
NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54		
NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16	*	+
NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28		
NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1		
NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83		
NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68		
NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62		
NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3		
NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33		
NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06		
NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33		
NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43		
NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46		
NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54		
NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06		
NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96		
NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87		
NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*	-
NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91		
NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4		
NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78		
NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28		
NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41		
NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	*	+
NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8		
NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14		
NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9		

NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93		
NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	*	+
NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59		
NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04		
NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15		
NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34		
NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**	-
NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59		
NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11		
NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55		
NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29		
NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44		
NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88		
NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56		
NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**	-
NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91		
NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3		
NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	*	+
NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74		
NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48		
NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71		
NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01		
NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88		
OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35		
OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05		
OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44		
OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73		
OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33		
OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17		

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OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72		
OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	*	+
OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36		
OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9		
OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6		
OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13		
OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42		
OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42		
OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04		
OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+



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OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
OVARC1000209	7.99	13.69	22.82	23.42	27.81	29.16		
OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
OVARC1000216	1.72	4.96	4.36	15.43	11.3	12.54	**	+
OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		

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OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		
OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+
OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		
OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		

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OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		
OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		
OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		

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OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		

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OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+
OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18		
OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76		
OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88		
OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48		
OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35		
OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49		
OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24		
OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28		
OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99		

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OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51		
OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9		
OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	*	+
OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14		
OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	*	+
OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22		
OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5		
OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53		
OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54		
OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16		
OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72		
OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56		
OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29		
OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86		
OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47		
OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54		
OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45		
OVARC1001030	96.19	101.41	143.98	119.24	154.26	133		
OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92		
OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77		
OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	*	+
OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25		
OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4		
OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84		
OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26		
OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49		
OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93		
OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	*	+
OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57		

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OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97		
OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52		
OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07		
OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79		
OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04		
OVARC1001078	2	5.12	2.79	3.57	3.08	2.83		
OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	**	+
OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13		
OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99		
OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05		
OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03		
OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22		
OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39		
OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67		
OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28		
OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	**	+
OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	**	+
OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66		
OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	**	+
OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84		
OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64		
OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89		
OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26		
OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54		
OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	*	+
OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06		
OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99		
OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51		
OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49		

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OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7		
OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56		
OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16		
OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96		
OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	*	+
OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9		
OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27		
OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62		
OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63		
OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65		
OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4		
OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86		
OVARC1001244	9.07	12.05	18	21.61	18.57	26.62		
OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	**	+
OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49		
OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85		
OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94		
OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16		
OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	*	-
OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26		
OVARC1001282	0.88	3.02	3.09	1.37	1.59	2		
OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41		
OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82		
OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32		
OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36		
OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22		
OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42		
OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02		
OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07		



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OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	**	+
OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3		
OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69		
OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78		
OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2		
OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69		
OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6		
OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62		
OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		
OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		
OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		

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OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		
OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		
OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		

OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		
OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		

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OVARC1001873	3.09	3.78	4.68	5.47	4.42	4.73		
OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+
OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53		
OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43		
OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63		
OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49		

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OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64		
OVARC1002092	1.38	2.72	2.2	4	3.97	1.88		
OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88		
OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	**	+
OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6		
OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92		
OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79		
OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52		
OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	*	+
OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09		
OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65		
OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51		
OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87		
OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64		
OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25		
OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12		
OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56		
PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	*	+
PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	*	+
PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67		
PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56		
PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55		
PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79		
PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56		
PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37		
PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74		
PLACE1000050	2.12	5.36	9.1	9	6.55	8.25		
PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37		
PLACE1000066	14.23	15	19.46	15.86	15.62	18.52		

PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11		
PLACE1000078	2.1	5.75	5	6.07	6.93	5.19		
PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27		
PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75		
PLACE1000094	0.7	4.18	1.72	1	3.44	2.96		
PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	*	+
PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39		
PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71		
PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24		
PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82		
PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78		
PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29		
PLACE1000181	1.06	3	2.98	2.63	3.75	2.86		
PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27		
PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03		
PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93		
PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09		
PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22		
PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1		
PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		

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PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		

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PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		
PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+



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PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		

PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		
PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		

PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		

PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		
PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		

PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9
PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08
PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71
PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7
PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32
PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81
PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28
PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71
PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56
PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7
PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85
PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88
PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52
PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37
PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38
PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1
PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49
PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02
PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09
PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85
PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13
PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83
PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13
PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32
PLACE1001716	1.68	3	2.61	2.24	3.79	3.58
PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71
PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51
PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36
PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16

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PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		
PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		

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PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		
PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		

PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		



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PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		
PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		
PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		

PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		

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PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		
PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		
PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81		
PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		

PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		
PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		
PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		

PLACE1003238	0.46	2.34	1.24	1.35	2	0.75		
PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89		
PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08		
PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87		
PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	*	+
PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64		
PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4		
PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3		
PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47		
PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09		
PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76		
PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97		
PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12		
PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98		
PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26		
PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	*	+
PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97		
PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62		
PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39		
PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89		
PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21		
PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08		
PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57		
PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27		
PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04		
PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04		
PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02		
PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7		
PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96		

PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42
PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99
PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84
PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61
PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17
PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79
PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86
PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24
PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2
PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08
PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81
PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87
PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39
PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75
PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19
PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4
PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88
PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22
PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83
PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3
PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93
PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23
PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58
PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04
PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48
PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15
PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23
PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65
PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53

PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55		
PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36		
PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25		
PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95		
PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68		
PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	**	+
PLACE1003611	2.34	5.18	6.07	5.65	7.14	6		
PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32		
PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8		
PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19		
PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86		
PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44		
PLACE1003638	1.3	2.58	3	5.21	4.19	3.13		
PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	*	+
PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4		
PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77		
PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11		
PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08		
PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76		
PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57		
PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42		
PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	*	+
PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44		
PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39		
PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16		
PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49		
PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29		
PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41		
PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85		

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PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	*	+
PLACE1003758	0.85	4.55	0.96	2	1.46	1.16		
PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79		
PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49		
PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11		
PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07		
PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43		
PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43		
PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	**	+
PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68		
PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32		
PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54		
PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92		
PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31		
PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86		
PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6		
PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39		
PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05		
PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92		
PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73		
PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69		
PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03		
PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	*	+
PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3		
PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68		
PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87		
PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6		
PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29		
PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59		



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PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84		
PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75		
PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32		
PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09		
PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78		
PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21		
PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57		
PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62		
PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15		
PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91		
PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	*	+
PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	*	+
PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45		
PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14		
PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71		
PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29		
PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93		
PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5		
PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01		
PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73		
PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12		
PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31		
PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53		
PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48		
PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2		
PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79		
PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76		
PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36		
PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84		

PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65		
PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35		
PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83		
PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64		
PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	*	+
PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93		
PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37		
PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64		
PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11		
PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65		
PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15		
PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82		
PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74		
PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04		
PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02		
PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49		
PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15		
PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1		
PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83		
PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12		
PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78		
PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52		
PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	*	+
PLACE1004325	2.43	6.38	3.84	3.85	3.66	4		
PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01		
PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71		
PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69		
PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03		
PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46		

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PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1		
PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67		
PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04		
PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	**	+
PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85		
PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58		
PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44		
PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24		
PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62		
PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	*	+
PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15		
PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37		
PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41		
PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39		
PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7		
PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88		
PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18		
PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	**	+
PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75		
PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48		
PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14		
PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21		
PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17		
PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15		
PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3		
PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82		
PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03		
PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18		
PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16		

PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22		
PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83		
PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	*	+
PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52		
PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09		
PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65		
PLACE1004547	5	7.61	7.82	8.66	11.2	10.28		
PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5		
PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15		
PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95		
PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82		
PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34		
PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49		
PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97		
PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99		
PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	*	+
PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17		
PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29		
PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59		
PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28		
PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22		
PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01		
PLACE1004658	2.4	7.34	6.31	6.64	8.37	6		
PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89		
PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14		
PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25		
PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39		
PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	*	+
PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72		

PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75
PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97
PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1
PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47
PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98
PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26
PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51
PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63
PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78
PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2
PLACE1004743	1.31	4.04	3.1	1.97	4	3.55
PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06
PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22
PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72
PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72
PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07
PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4
PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25
PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88
PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22
PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45
PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1
PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44
PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84
PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85
PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3
PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49
PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68
PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37

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PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		
PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		
PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		

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PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		
PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		
PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		

PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+
PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		



PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		
PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46		
PLACE1005477	1.58	2.26	2.51	3	2.93	2.74		
PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53		
PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44		
PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06		
PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62		
PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91		
PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49		
PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49		
PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98		
PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78		
PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83		
PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71		

PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33		
PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67		
PLACE1005536	1.74	1	2.74	3.12	2.43	2.88		
PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22		
PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57		
PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27		
PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86		
PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17		
PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7		
PLACE1005563	0.51	4	1.89	1.45	2.07	1.06		
PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09		
PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22		
PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03		
PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02		
PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89		
PLACE1005601	2	5.66	4.22	3.77	4	4.02		
PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94		
PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46		
PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89		
PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26		
PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61		
PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	**	+
PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18		
PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55		
PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25		
PLACE1005648	3	8.11	9.21	8.34	10.59	8.22		
PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67		
PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58		
PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32		

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PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34		
PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19		
PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97		
PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6		
PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47		
PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38		
PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76		
PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29		
PLACE1005727	2.97	4.54	4.15	3.9	3.49	4		
PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28		
PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		

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PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		

PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		
PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		
PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		
PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		

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PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		
PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		
PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		

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PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		

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PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		
PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		



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PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
PLACE1006860	1	4.29	1.62	1.61	2.1	1		
PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		

PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		
PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		

PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+

PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		
PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51		
PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8		
PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02		
PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52		
PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	*	+
PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91		
PLACE1007450	0.79	1.22	2.65	3	2.99	2.39		
PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45		
PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61		
PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58		
PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92		
PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69		
PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46		
PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11		
PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42		
PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9		
PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96		
PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24		
PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1		
PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61		

PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4		
PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41		
PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59		
PLACE1007565	0.37	2.27	1	1	1.16	0.91		
PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	**	+
PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09		
PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07		
PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71		
PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5		
PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41		
PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38		
PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53		
PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63		
PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37		
PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95		
PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13		
PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9		
PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4		
PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91		
PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98		
PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61		
PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8		
PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08		
PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75		
PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49		
PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39		
PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99		
PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32		
PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17		

PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03		
PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97		
PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94		
PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58		
PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17		
PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87		
PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29		
PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27		
PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3		
PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44		
PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06		
PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39		
PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39		
PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86		
PLACE1007845	1.76	3	4.11	3.45	3.42	2.36		
PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5		
PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25		
PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24		
PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	**	+
PLACE1007866	19.42	25.98	40.48	43	80.39	56.73		
PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08		
PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53		
PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9		
PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93		
PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01		
PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41		
PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24		
PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54		
PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94		

PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63		
PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51		
PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05		
PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22		
PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8		
PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17		
PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21		
PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92		
PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88		
PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66		
PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51		
PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02		
PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16		
PLACE1008045	0.4	4.07	1.54	1.75	2	1.65		
PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78		
PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86		
PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23		
PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74		
PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68		
PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04		
PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	*	+
PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5		
PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91		
PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63		
PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8		
PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46		
PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		

PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		



PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		
PLACE1008532	2.12	3	5.51	5.66	4.72	4.19		
PLACE1008533	2.01	4	4.07	5.53	5.18	3.77		
PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72		
PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53		
PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47		
PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38		
PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21		
PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6		
PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31		

PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57		
PLACE1008603	5.9	7.25	31	30.55	43.67	29.76		
PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16		
PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03		
PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95		
PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7		
PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41		
PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51		
PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94		
PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24		
PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91		
PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13		
PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2		
PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		

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PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		
PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		
PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		
PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		

PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		
PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		
PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		

PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		
PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		

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PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
PLACE1009731	1.36	3.59	3	3.58	6.53	5		
PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		

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PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		
PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68		
PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39		
PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75		
PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89		
PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74		
PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03		
PLACE1009798	1.59	5.37	4	6.26	5.57	5.67		
PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92		
PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59		
PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56		
PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11		
PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73		
PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32		
PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34		
PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72		
PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94		
PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9		
PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15		
PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47		
PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57		
PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04		
PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5		
PLACE1009931	2.78	5.21	9	8.71	6.93	8.09		
PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5		
PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03		
PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9		
PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45		

PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96		
PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68		
PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23		
PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64		
PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46		
PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68		
PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68		
PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06		
PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14		
PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82		
PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19		
PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64		
PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37		
PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05		
PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3		
PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09		
PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22		
PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82		
PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85		
PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*	+
PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26		
PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48		
PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2		
PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57		
PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82		
PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		



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PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		

PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		
PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		

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PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		
PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5		
PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29		
PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67		
PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*	+
PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22		
PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61		
PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75		
PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2		
PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25		
PLACE1010713	7	10.81	14.7	9.14	8.16	15.14		
PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47		
PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93		
PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61		
PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49		
PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93		
PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21		
PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53		
PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08		
PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42		
PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34		
PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21		
PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17		
PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93		
PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3		
PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18		

PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7		
PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81		
PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09		
PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13		
PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59		
PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56		
PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94		
PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62		
PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51		
PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95		
PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47		
PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85		
PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2		
PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		
PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		

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PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		
PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		

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PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		
PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		
PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		

PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		
PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		
PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		

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PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		
PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		
PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		



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PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		
PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
PLACE2000003	1.18	3.64	6.86	7.38	8.12	8.92		
PLACE2000005	1.16	2.41	2.16	2.76	2.03	1.89		
PLACE2000006	2.52	4.13	15.6	11.34	16.58	13.4		
PLACE2000007	0.96	4.85	4.24	3.94	5.13	3.33		
PLACE2000011	1.72	3.27	3.34	4.3	5.06	3.62		
PLACE2000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
PLACE2000015	1.27	4.79	3.52	2.77	3.31	2.69		
PLACE2000017	0.48	4.78	2.15	2.65	2.56	2.45		
PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61		
PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71		
PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97		
PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32		
PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37		

PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05

PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42		
PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19		
PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68		
PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3		
PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56		
PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48		
PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47		
PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97		
PLACE2000246	1.93	2	6.06	4.58	5.09	3.93		
PLACE2000264	0.67	1.39	1.85	2.45	3.74	3	*	+
PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1		
PLACE2000287	0.81	4.44	1.49	2	2.59	1.34		
PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69		
PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45		
PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02		
PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4		
PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3		
PLACE2000334	3.52	5	6.6	7.33	8.12	5.88		
PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		

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PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+
PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		
PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		

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PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		
PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		
PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		
PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		

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PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		
PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		

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PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		
PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29		
PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22		
PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05		
PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82		
PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	*	+
PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79		
PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01		
PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42		
PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52		
PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72		
PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92		
PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14		
PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91		
PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21		
PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42		
PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31		
PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84		
PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82		
PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19		
PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25		
PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91		
PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86		
PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02		

PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71
PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73
PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84
PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98
PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94
PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9
PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21
PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4
PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78
PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22
PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61
PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07
PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84
PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76
PLACE4000192	1.3	2.27	3.6	2.36	2	1.25
PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02
PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44
PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69
PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5
PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38
PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48
PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15
PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51
PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35
PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35
PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8
PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64
PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02
PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12



PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51		
PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85		
PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59		
PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87		
PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	*	+
PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21		
PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82		
PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59		
PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18		
PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	*	+
PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79		
PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38		
PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82		
PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07		
PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12		
PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63		
PLACE4000399	10.99	17.08	75.17	59.11	80.22	58		
PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4		
PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87		
PLACE4000411	2.22	2.28	4	2.27	2.6	1.82		
PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78		
PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83		
PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51		
PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79		
PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14		
PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27		
PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04		
PLACE4000455	5.18	7.39	9.55	8	7.21	4.63		
PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34		

PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31		
PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22		
PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05		
PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69		
PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08		
PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37		
PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2		
PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11		
PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22		
PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32		
PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15		
PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44		
PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25		
PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83		
PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74		
PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58		
PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16		
PLACE4000651	2.42	6.4	7.48	5	7.01	6.07		
PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47		
PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67		
PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77		
PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12		
PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07		
PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76		
PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79		
PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32		
PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09		
PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	*	+
PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84		

PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87		
PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54		
PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64		
PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73		
PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57		
PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8		
PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87		
PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82		
SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96		
SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77		
SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44		
SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96		
SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44		
SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56		
SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55		
SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12		
SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73		
SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92		
SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39		
SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	**	+
SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18		
SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43		
SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89		
SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67		
SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1		
SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11		
SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02		
SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3		
SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88		

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SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26		
SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52		
SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99		
SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84		
SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99		
SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68		
SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47		
SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64		
SPLEN1000072	1	8.5	4.7	2.82	3	2.21		
SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63		
SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76		
SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04		
SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32		
SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99		
SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52		
SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8		
SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51		
SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61		
SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68		
SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15		
SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67		
SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95		
THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6		
THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1		
THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	*	+
THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38		
THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6		
THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14		
THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31		

THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45		
THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28		
THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23		
THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11		
THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55		
THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04		
THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74		
THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94		
THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	*	+
THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74		
THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27		
THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93		
THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97		
THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66		
THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11		
THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36		
THYRO1000034	0.49	4.16	1.59	1.99	2	1.82		
THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11		
THYRO1000036	0.93	8.32	4	3.08	4.36	5.59		
THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93		
THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61		
THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3		
THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45		
THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06		
THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42		
THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85		
THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15		
THYRO1000087	0.72	3.86	1.01	0	0.58	0.17		
THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5		

THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95		
THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39		
THYRO1000107	0.5	2.95	2.7	2.86	3.22	2		
THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36		
THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95		
THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64		
THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92		
THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39		
THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26		
THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73		
THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33		
THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		

THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
THYRO1000501	1.12	4.01	2.78	3	1.92	1.82		

THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		
THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88		
THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49		
THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42		
THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78		
THYRO1000577	1.06	5	1.34	0.96	1.22	0.71		
THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79		
THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58		
THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52		
THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21		
THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97		
THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56		
THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29		
THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78		
THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67		
THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54		
THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64		
THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86		
THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09		
THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66		
THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43		
THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56		
THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53		
THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47		
THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59		



THYR01000699	2.98	2.14	5.55	4.86	7.08	7.12
THYR01000712	1.88	4.25	5.9	6.25	6.75	7.78
THYR01000715	5.74	5.67	27.37	21.74	28.63	16.99
THYR01000716	0.92	3.26	3.2	1.88	1.78	1.35
THYR01000717	1.58	5	4.36	2.98	4.63	1.91
THYR01000723	0.6	4.54	1.6	0.55	1.06	0.85
THYR01000734	-0.01	4.81	1.89	1.49	1.73	1.07
THYR01000748	0.98	5.51	5.23	2.35	3.85	3.18
THYR01000755	1.74	3.26	4.32	4.33	3.47	4.38
THYR01000756	2.79	4.24	3.24	3.46	4.2	3.41
THYR01000776	0.48	2.17	3.02	3.36	3.99	3.34
THYR01000777	1.81	3.39	4.54	4.99	2.05	2.37
THYR01000779	1.45	3.55	0.88	0.18	1.01	-0.26
THYR01000782	3.92	10.13	12.52	10.76	15.05	14.05
THYR01000783	0.12	5.51	1.2	1.11	1.41	0.92
THYR01000786	6.65	9.54	19.71	15.74	7.92	13.7
THYR01000787	0.23	1.88	1.67	1.31	1.54	0.78
THYR01000792	1.51	3.13	2.29	3.09	3.13	2.11
THYR01000793	0.11	3.13	0.84	1.51	1.86	1.16
THYR01000795	1.23	6.03	3.54	2.76	3.1	3.05
THYR01000796	0.6	7.73	2.44	2.26	2.95	1.66
THYR01000798	1.89	5.82	2.51	2.59	3.57	3.53
THYR01000800	9.26	17.2	24.74	17.74	20.68	21.06
THYR01000805	0.49	3.04	1.08	0.72	2.66	1.38
THYR01000815	2.54	3.49	9.48	7.61	5.47	7.87
THYR01000829	5.55	7.83	10.57	3.78	8.32	10.01
THYR01000835	0.96	3.2	1.93	1.07	2.36	1.8
THYR01000843	1.09	11.48	3.56	3.69	4.41	3.62
THYR01000846	0.76	5.71	1.32	2.67	1.62	1.26

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THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32		
THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	*	+
THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95		
THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01		
THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	*	+
THYRO1000894	0.33	3.95	1.36	1.75	1.48	1		
THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82		
THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29		
THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89		
THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82		
THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46		
THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9		
THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24		
THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87		
THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48		
THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64		
THYRO1000964	0.42	11.59	0.76	1	1.27	1.06		
THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19		
THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71		
THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68		
THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12		
THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26		
THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67		
THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2		
THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26		
THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56		
THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66		
THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24		
THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41		

THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16		
THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02		
THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62		
THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84		
THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76		
THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78		
THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5		
THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78		
THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93		
THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18		
THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99		
THYRO1001113	11.41	17.42	32	21.81	26.65	18.72		
THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72		
THYRO1001121	1.57	4.28	4.19	3.92	2.72	3		
THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09		
THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12		
THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38		
THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22		
THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62		
THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52		
THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97		
THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94		
THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31		
THYRO1001204	2.17	3.58	4.27	4.03	4.74	4		
THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9		
THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33		
THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	*	+
THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46		
THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46		

THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66
THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69
THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66
THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97
THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2
THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36
THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5
THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18
THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5
THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48
THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83
THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23
THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01
THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49
THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18
THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65
THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1
THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28
THYRO1001365	0.86	3	1.6	2.19	2.6	1.96
THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21
THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29
THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94
THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63
THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36
THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12
THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87
THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18
THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81
THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73

THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4
THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67
THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23
THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21
THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64
THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75
THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57
THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13
THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48
THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55
THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6
THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35
THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54
THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38
THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51
THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26
THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52
THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98
THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54
THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23
THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73
THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16
THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54 * +
THYRO1001563	9.49	14.06	15.89	10	15.49	22.09
THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41
THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67
THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29
THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52
THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29

THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51		
THYRO1001602	1.49	3.26	3.52	4.95	5.22	3.41		
THYRO1001605	1.58	4.48	3.22	3.2	3.43	2.42		
THYRO1001608	1.87	9.45	5.1	5.04	8.23	4.7		
THYRO1001617	6.06	13.68	11.47	9.75	10.87	9.61		
THYRO1001634	1.87	9.08	3.46	2.93	5.59	2.05		
THYRO1001637	3.51	3.13	9.65	8.72	7.94	9.07		
THYRO1001641	2.57	3.73	5.09	4.03	3.08	2.94		
THYRO1001656	1.59	2.94	4.16	2.82	5.36	2.33		
THYRO1001658	22.34	29.19	40.11	34.98	33.16	42.01		
THYRO1001661	1.4	5.83	2.31	2.93	3.31	2.05		
THYRO1001671	0.67	7.36	2.68	1.89	1.34	1.8		
THYRO1001672	1.1	9.24	2.1	1.14	1.52	1.66		
THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16		
THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36		
THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72		
THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37		
THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29		
THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21		
THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53		
THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77		
THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29		
THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8		
THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78		
THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06		
THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27		
THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88		
THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17	*	+
THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06		

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THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25	*	+
THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92		
THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24	*	+
THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09		
THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42		
THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39		
THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27		
THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77		
THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55		
THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31		
THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28		
THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74		
TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22		
TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65		
TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77		
TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11		
TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65		
TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09		
TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54		
TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75		
TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72		
TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69		
VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02		
VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94		
VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88		
VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	*	+
VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27		
VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59		
VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48		

VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79		
VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5		
VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65		
VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27		
VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87		
VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	*	+
VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59		
VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7		
VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36		
VESEN1000410	1.11	5	1.78	2.36	2.71	3.69		
VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	*	+
VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29		
VESEN1000440	7	5.53	7.81	3.79	9.4	12.22		
VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11		
VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	*	+
VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58		
VESEN1000557	4.22	7.94	7.73	6.55	9.07	10		
VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8		
VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08		
VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46		
VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91		
VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51		
VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21		
VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96		
VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	*	+
VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1		
VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61		
VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66		
VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59		



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VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47		
VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12		
VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6		
VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33		
VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
VESEN2000272	2.29	4	8.92	7	8.31	5.88		
VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		

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VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		
Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		

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Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		
Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		

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Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		
Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45		
Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22		
Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17		
Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31		
Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97		
Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	**	+
Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18		
Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45		

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Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7		
Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	**	+
Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95		
Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71		
Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94		
Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56		
Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62		
Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38		
Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21		
Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11		
Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01		
Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44		
Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96		
Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	**	+
Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23		
Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39		
Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1		
Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6		
Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	*	+
Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56		
Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79		
Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14		
Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	**	+
Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	*	+
Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21		
Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51		
Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59		
Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	**	+
Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48		

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Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68		
Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	*	+
Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07		
Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79		
Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13		
Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1		
Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3		
Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	*	+
Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41		
Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43		
Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56		
Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89		
Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	*	+
Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23		
Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	*	+
Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+

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Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		
Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		

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Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		
Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94		
Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2		
Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94		
Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14		
Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25		
Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	*	+
Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82		
Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53		
Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	**	+
Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	*	+
Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57		
Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46		
Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47		
Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1		
Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	**	+
Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	*	+
Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19		
Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34		
Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1		
Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	*	+



Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83		
Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54		
Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05		
Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02		
Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73		
Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66		
Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66		
Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67		
Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65		
Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73		
Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75		
Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35		
Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51		
Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55		
Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85		
Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21		
Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14		
Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43		
Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77		
Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33		
Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24		
Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28		
Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42		
Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15		
Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35		
Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8		
Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	*	+
Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9		
Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33		

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Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17		
Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15		
Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79		
Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		
Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51		
Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		
Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		

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Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		
Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		
Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6		
Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		
Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		

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Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		

Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

## 【 0 8 1 0 】

実施例 1 6. オリゴキャップ法で作製された cDNA ライブラリーからの新規 cDNA クロンの選抜

オリゴキャップ法で作製された cDNA ライブラリーから得られたクローンの 5' 末端配列中に開始コドンから始まる 50 アミノ酸以上のタンパク質コード領域が推定される 54 クローン、HEMBA1000497、HEMBA1001750、HEMBA1003854、HEMBA1004193、HEMBA1004860、HEMBA1005572、HEMBA1006038、HEMBA1006092、HEMBA1006406、HEMBA1006650、HEMBA1006812、HEMBB1000672、HEMBB1001197、HEMBB1001871、MAMMA1001252、MAMMA1002094、NT2RM4000634、NT2RM4000657、NT2RM4000783、NT

2RM4000857、NT2RM4001178、NT2RM4002420、NT2RP2000198、NT2RP2000551、NT2RP2000660、NT2RP2001214、NT2RP2001460、NT2RP2001756、NT2RP2002056、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2003101、NT2RP2003799、NT2RP2004095、NT2RP2004732、NT2RP2004920、NT2RP2005454、NT2RP2005776、NT2RP2005806、NT2RP2005882、NT2RP3001282、NT2RP3001723、NT2RP3002099、NT2RP3003155、NT2RP3004028、OVARC1000008、OVARC1000724、OVARC1000751、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218を新たに選抜した。

中でもHEMBA1000497、HEMBA1003854、HEMBA1004193、HEMBA1006812、HEMBB1001871、NT2RM4000657、NT2RM4001178、NT2RP2001756、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2004095、NT2RP2004920、NT2RP2005806、NT2RP3001282、NT2RP3002099、NT2RP3003155、OVARC1000724、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218の23クローンは100アミノ酸以上のタンパク質コード領域が推定され、タンパク質コード領域を含む確率が非常に高いことが示された。

# 【 0 8 1 1 】

各クローンの最大ATGpr1値を表 4 5 3 に示す。HEMBA1006812、HEMBB1001871、NT2RP3001282は最大ATGpr1値が0.3より大であるため全長である確率が高いが、その他HEMBA1000497、HEMBA1001750、HEMBA1003854、HEMBA1004193、HEMBA1004860、HEMBA1005572、HEMBA1006038、HEMBA1006092、HEMBA1006406、HEMBA1006650、HEMBB1000672、HEMBB1001197、MAMMA1001252、MAMMA1002094、NT2RM4000634、NT2RM4000657、NT2RM4000783、NT2RM4000857、NT2RM4001178、NT2RM4002420、NT2RP2000198、NT2RP2000551、NT2RP2000660、NT2RP2001214、NT2RP2001460、NT2RP2001756、NT2RP2002056、NT2RP2002677、NT2RP2002755、NT2RP2002843、NT2RP2003101、NT2RP2003799、NT2RP2004095、NT2RP2004732、NT2RP2004920、NT2RP2005454、NT2RP2005776、NT2RP2005806、NT2RP2005882、NT2RP3001723、NT2RP3002099、NT2RP3003155、NT2RP3004028、OVARC1000008、OVARC1000724、OVARC1000751、OVARC1001029、PLACE1000814、PLACE1003030、PLACE1005549、PLACE1007218は最大ATGpr1値が0.3以下であるため全長率が低いとされるものの依然全長である可能性はある。

表 4 5 4 (表 2 と同じ内容を表す) 中に 5 4 クローンにおける 5' 側と 3' 側を規定する塩基配列を示す配列番号と、そのポリヌクレオチドをインサートとして含む実施例で取得したプラスミドクロンの対応関係を示す。5' 配列 配列名の右側が 5' 配列の配列番号であり、3' 配列 配列名の右側が 3' 配列の配列番号である。

選抜された 54 クローンの 5' 末端配列を Swiss-Prot に対して、5' 末端配列、3' 末端配列を GenBank、UniGene に対して相同性検索した。それぞれの検索結果は、明細書の最後に相同性検索結果データ 7 ~ 1 1 として示した。

#### 【 0 8 1 2 】

得られたトップヒットデータからは、少なくとも、分泌・膜タンパク質、糖タンパク質、シグナル伝達関連タンパク質、転写関連タンパク質、疾患関連タンパク質、タンパク質合成・輸送関連タンパク質のいずれかのカテゴリーに属するタンパク質をコードすると推定されるクロンが 7 クローンあった。いずれも該カテゴリーに属する既知タンパク質と比較的相同性の低いとされるクロンであった。ここでいう「比較的相同性が低い」とは、「比較的相同性が高い」条件 (Swiss-Prot データベースの既知配列との比較において、Identity が 60% 以上、かつ P 値が  $10^{-10}$  以下のスコアである) は満たさないが、Swiss-Prot データベースの既知配列との比較において、比較配列の長さが 55 塩基以上、かつ Identity が 25% 以上、かつ P 値が  $10^{-6}$  以下のスコアであることを示す。

7 クローンのうち、分泌・膜タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクロンは HEMBB1001871, NT2RM4000857 の 2 クローンであった (他のカテゴリーに重複して属するクロン)。糖タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクロンは HEMBB1001871, NT2RM4000857 の 2 クローンであった (他のカテゴリーに重複して属するクロン)。シグナル伝達関連タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクロンは PLACE1005549 の 1 クローンであった。転写関連タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクロンは HEMBA1005572, NT2RP2001756, NT2RP2005776 の 3 クローンであった。疾患関連タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクロンは NT2RM4000857

の1クローンであった（他のカテゴリーに重複して属するクローン）。タンパク質合成・輸送関連タンパク質のカテゴリーに属するタンパク質をコードすると推定されるクローンはHEMBA1001750の1クローンであった（実施例 1 2 . 参照）。

【 0 8 1 3 】

【 表 4 5 4 】

実施例 1 6 で選抜されたクローンの最大ATGpr1値

クローン名	配列名	最大 ATGpr1値
HEMBA1000497	F-HEMBA1000497	0.25
HEMBA1001750	F-HEMBA1001750	0.08
HEMBA1003854	F-HEMBA1003854	0.23
HEMBA1004193	F-HEMBA1004193	0.22
HEMBA1004860	F-HEMBA1004860	0.29
HEMBA1005572	F-HEMBA1005572	0.24
HEMBA1006038	F-HEMBA1006038	0.29
HEMBA1006092	F-HEMBA1006092	0.28
HEMBA1006406	F-HEMBA1006406	0.26
HEMBA1006650	F-HEMBA1006650	0.22
HEMBA1006812	F-HEMBA1006812	0.71
HEMBB1000672	F-HEMBB1000672	0.24
HEMBB1001197	F-HEMBB1001197	0.22
HEMBB1001871	F-HEMBB1001871	0.94
MAMMA1001252	F-MAMMA1001252	0.29
MAMMA1002094	F-MAMMA1002094	0.28
NT2RM4000634	F-NT2RM4000634	0.07
NT2RM4000657	F-NT2RM4000657	0.24
NT2RM4000783	F-NT2RM4000783	0.22



NT2RM4000857	F-NT2RM4000857	0.12
NT2RM4001178	F-NT2RM4001178	0.27
NT2RM4002420	F-NT2RM4002420	0.06
NT2RP2000198	F-NT2RP2000198	0.15
NT2RP2000551	F-NT2RP2000551	0.07
NT2RP2000660	F-NT2RP2000660	0.22
NT2RP2001214	F-NT2RP2001214	0.26
NT2RP2001460	F-NT2RP2001460	0.07
NT2RP2001756	F-NT2RP2001756	0.17
NT2RP2002056	F-NT2RP2002056	0.12
NT2RP2002677	F-NT2RP2002677	0.14
NT2RP2002755	F-NT2RP2002755	0.12
NT2RP2002843	F-NT2RP2002843	0.11
NT2RP2003101	F-NT2RP2003101	0.13
NT2RP2003799	F-NT2RP2003799	0.24
NT2RP2004095	F-NT2RP2004095	0.16
NT2RP2004732	F-NT2RP2004732	0.18
NT2RP2004920	F-NT2RP2004920	0.15
NT2RP2005454	F-NT2RP2005454	0.09
NT2RP2005776	F-NT2RP2005776	0.19
NT2RP2005806	F-NT2RP2005806	0.27
NT2RP2005882	F-NT2RP2005882	0.11
NT2RP3001282	F-NT2RP3001282	0.39
NT2RP3001723	F-NT2RP3001723	0.22
NT2RP3002099	F-NT2RP3002099	0.20
NT2RP3003155	F-NT2RP3003155	0.29
NT2RP3004028	F-NT2RP3004028	0.13
OVARC1000008	F-OVARC1000008	0.23
OVARC1000724	F-OVARC1000724	0.27

OVARC1000751	F-OVARC1000751	0.28
OVARC1001029	F-OVARC1001029	0.25
PLACE1000814	F-PLACE1000814	0.21
PLACE1003030	F-PLACE1003030	0.26
PLACE1005549	F-PLACE1005549	0.16
PLACE1007218	F-PLACE1007218	0.30

【 0 8 1 4 】

【表 4 5 5】

クローン名	5' 末端配列 配列名	5' 末端 配列番号	3' 末端配列 配列名	3' 末端 配列番号
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175
HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180

NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209

NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

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#### 【 0 8 1 5 】

実施例 1 7 . 推定アミノ酸配列に対するシグナル配列、膜貫通領域および機能ドメインの検索

全長塩基配列から推定されたアミノ酸配列に対して、アミノ末端のシグナル配列の有無と膜貫通領域の有無を予測、さらにタンパク質の機能ドメイン（モチーフ）検索を行った。アミノ末端のシグナル配列についてはPSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)] を、膜貫通領域についてはSOSUI [T. Hirokawa et.al. Bioinformatics, 14: 378-379 (1998)]（三井情報開発株式会社販売）を用いて解析を行った。機能ドメインの検索についてはPfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) を用いた。PSORTやSOSUIにより、アミノ末端のシグナル配列や膜貫通領域が予測されたアミノ酸配列は分泌、膜タンパク質であると予測された。また、Pfamによる機能ドメイン検索において、ある機能ドメインにヒットしたアミノ酸配列はヒットデータをもとに、例えばPROSITE(<http://www.expasy.ch/cgi-bin/prosite-list.pl>)にある機能カテゴリー分類を参照にしてそのタンパク質の機能予測することができる。また、PROSITEでの機能ドメインの検索も可能である。

各ソフトウェアによる検索結果を以下に示す。

#### 【 0 8 1 6 】

PSORTにより推定アミノ酸配列にシグナル配列を検出されたクローンは、以下

の通りであった。

HEMBA1001052, HEMBA1001407, HEMBA1002486, HEMBA1002661, HEMBA1002818, HEMBA1002876, HEMBA1003086, HEMBA1003711, HEMBA1004752, HEMBA1005991, HEMBA1006067, HEMBA1006173, HEMBA1006198, HEMBA1006789, HEMBA1006921, HEMBB1000054, HEMBB1000175, HEMBB1002692, MAMMA1000798, MAMMA1002427, MAMMA1002881, MAMMA1003035, NT2RM1000035, NT2RM1000742, NT2RM1000811, NT2RM1000905, NT2RM1001008, NT2RM2000287, NT2RM2000609, NT2RM2001613, NT2RM4000634, NT2RM4000778, NT2RM4002339, NT2RM4002460, NT2RP1000782, NT2RP1000856, NT2RP1001247, NT2RP1001546, NT2RP1001569, NT2RP2001597, NT2RP2002537, NT2RP2004142, NT2RP2005752, NT2RP2005812, NT2RP3001084, NT2RP3001589, NT2RP3002163, NT2RP3002650, NT2RP3003145, NT2RP3003242, NT2RP3003621, NT2RP3004282, NT2RP3004503, NT2RP4000051, NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000417, NT2RP4001064, NT2RP4001117, NT2RP4001730, NT2RP4001739, NT2RP4002075, NT2RP5003500, OVARC1001154, PLACE1000611, PLACE1003030, PLACE1003044, PLACE1003369, PLACE1003596, PLACE1004258, PLACE1005086, PLACE1006239, PLACE1006754, PLACE1006829, PLACE1007954, PLACE1008424, PLACE1008533, PLACE1008693, PLACE1010622, PLACE1010942, PLACE2000176, PLACE2000341, PLACE2000379, PLACE2000427, PLACE2000477, PLACE4000431, PLACE4000593, THYRO1000156, THYRO1001134, THYRO1001287, Y79AA1000258, Y79AA1001874, Y79AA1002399

【 0 8 1 7 】

SOSUIにより推定アミノ酸配列に膜貫通領域を検出されたクローンは、以下の通りであった。

HEMBA1000005, HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719, HEMBA1000817, HEMBA1000822, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001085, HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001510, HEMBA1001515, HEMBA1001557, HEMBA1001746, HEMBA1002092, HEMBA1002125, HEMBA1002150, HEMBA1002166, HEMBA1002462, HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661, HEMBA1002780

, HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003077, HEMBA1003079, HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003711, HEMBA1003742, HEMBA1003803, HEMBA1004143, HEMBA1004146, HEMBA1004341, HEMBA1004461, HEMBA1004577, HEMBA1004637, HEMBA1004752, HEMBA1004756, HEMBA1004850, HEMBA1004889, HEMBA1004923, HEMBA1004930, HEMBA1005029, HEMBA1005035, HEMBA1005050, HEMBA1005552, HEMBA1005588, HEMBA1005616, HEMBA1005991, HEMBA1006036, HEMBA1006067, HEMBA1006293, HEMBA1006492, HEMBA1006502, HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926, HEMBA1007203, HEMBB1000050, HEMBB1000054, HEMBB1000556, HEMBB1000593, HEMBB1000631, HEMBB1000763, HEMBB1000827, HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001177, HEMBB1001302, HEMBB1001348, HEMBB1001962, HEMBB1002142, HEMBB1002190, HEMBB1002247, HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692, MAMMA1000129, MAMMA1000133, MAMMA1000277, MAMMA1000278, MAMMA1000410, MAMMA1000416, MAMMA1000472, MAMMA1000714, MAMMA1000731, MAMMA1000734, MAMMA1000798, MAMMA1000842, MAMMA1000956, MAMMA1001008, MAMMA1001030, MAMMA1001139, MAMMA1001154, MAMMA1001388, MAMMA1001411, MAMMA1001487, MAMMA1001751, MAMMA1001771, MAMMA1002461, MAMMA1002524, MAMMA1002598, MAMMA1002684, MAMMA1002769, MAMMA1002890, MAMMA1002938, MAMMA1003146, NT2RM1000035, NT2RM1000037, NT2RM1000062, NT2RM1000131, NT2RM1000257, NT2RM1000260, NT2RM1000355, NT2RM1000648, NT2RM1000742, NT2RM1000800, NT2RM1000811, NT2RM1000857, NT2RM1000867, NT2RM1000882, NT2RM1001008, NT2RM1001115, NT2RM1001139, NT2RM2000259, NT2RM2000395, NT2RM2000402, NT2RM2000407, NT2RM2000422, NT2RM2000566, NT2RM2000581, NT2RM2000609, NT2RM2001370, NT2RM2001393, NT2RM2001499, NT2RM2001613, NT2RM2001648, NT2RM2001659, NT2RM2001671, NT2RM2001718, NT2RM2001760, NT2RM2001785, NT2RM2001823, NT2RM2001930, NT2RM2001950, NT2RM2001998, NT2RM2002049, NT2RM4000046, NT2RM4000233, NT2RM4000433, NT2RM4000520, NT2RM4000634, NT2RM4000674, NT2RM4000700, NT2RM4000764, NT2RM4000795, NT2RM4000820, NT2RM4000857, NT2RM4001032, NT2RM4001054, NT

2RM4001455, NT2RM4001813, NT2RM4001930, NT2RM4001987, NT2RM4002054, NT2RM4002073, NT2RM4002145, NT2RM4002146, NT2RM4002194, NT2RM4002339, NT2RM4002438, NT2RM4002446, NT2RM4002452, NT2RM4002460, NT2RM4002493, NT2RM4002571, NT2RP1000191, NT2RP1000358, NT2RP1000418, NT2RP1000547, NT2RP1000609, NT2RP1000677, NT2RP1000767,

【 0 8 1 8 】

NT2RP1000782, NT2RP1000856, NT2RP1001113, NT2RP1001247, NT2RP1001286, NT2RP1001310, NT2RP1001311, NT2RP1001313, NT2RP1001385, NT2RP1001449, NT2RP1001546, NT2RP1001569, NT2RP2000032, NT2RP2000040, NT2RP2000070, NT2RP2000091, NT2RP2000114, NT2RP2000120, NT2RP2000173, NT2RP2000175, NT2RP2000195, NT2RP2000248, NT2RP2000270, NT2RP2000283, NT2RP2000289, NT2RP2000459, NT2RP2000516, NT2RP2000842, NT2RP2000892, NT2RP2001081, NT2RP2001268, NT2RP2001295, NT2RP2001366, NT2RP2001576, NT2RP2001581, NT2RP2001597, NT2RP2001947, NT2RP2001991, NT2RP2002025, NT2RP2002312, NT2RP2002385, NT2RP2002479, NT2RP2002537, NT2RP2002643, NT2RP2002701, NT2RP2002740, NT2RP2002857, NT2RP2003125, NT2RP2003297, NT2RP2003433, NT2RP2003446, NT2RP2003466, NT2RP2003629, NT2RP2003777, NT2RP2003781, NT2RP2004041, NT2RP2004194, NT2RP2004270, NT2RP2004681, NT2RP2004775, NT2RP2004799, NT2RP2004936, NT2RP2005012, NT2RP2005159, NT2RP2005227, NT2RP2005270, NT2RP2005344, NT2RP2005509, NT2RP2005752, NT2RP2005781, NT2RP2005784, NT2RP2005812, NT2RP2006069, NT2RP2006100, NT2RP2006141, NT2RP2006261, NT2RP2006571, NT2RP3000092, NT2RP3000134, NT2RP3000333, NT2RP3000393, NT2RP3000439, NT2RP3000441, NT2RP3000531, NT2RP3000685, NT2RP3000826, NT2RP3000852, NT2RP30001126, NT2RP3001176, NT2RP3001260, NT2RP3001355, NT2RP3001383, NT2RP3001426, NT2RP3001453, NT2RP3001497, NT2RP3001538, NT2RP3001716, NT2RP3001727, NT2RP3001739, NT2RP3001799,

【 0 8 1 9 】

NT2RP3001943, NT2RP3001944, NT2RP3002002, NT2RP3002014, NT2RP3002054, NT2RP3002108, NT2RP3002163, NT2RP3002351, NT2RP3002455, NT2RP3002549, NT2R

P3002628, NT2RP3002650, NT2RP3002687, NT2RP3002701, NT2RP3002869, NT2RP3002969, NT2RP3003008, NT2RP3003071, NT2RP3003101, NT2RP3003145, NT2RP3003302, NT2RP3003353, NT2RP3003409, NT2RP3003716, NT2RP3003918, NT2RP3004207, NT2RP3004454, NT2RP3004503, NT2RP4000051, NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000500, NT2RP4000560, NT2RP4000588, NT2RP4000713, NT2RP4000724, NT2RP4000833, NT2RP4000878, NT2RP4000907, NT2RP4000925, NT2RP4000928, NT2RP4000973, NT2RP4000989, NT2RP4001057, NT2RP4001064, NT2RP4001079, NT2RP4001117, NT2RP4001138, NT2RP4001150, NT2RP4001174, NT2RP4001274, NT2RP4001345, NT2RP4001372, NT2RP4001373, NT2RP4001379, NT2RP4001498, NT2RP4001547, NT2RP4001571, NT2RP4001644, NT2RP4001677, NT2RP4001803, NT2RP4001822, NT2RP4001975, NT2RP4002052, NT2RP4002075, NT2RP5003500, NT2RP5003506, NT2RP5003522, NT2RP5003534, OVARC1000151, OVARC1000241, OVARC1000335, OVARC1000700, OVARC1000722, OVARC1000751, OVARC1000850, OVARC1000924, OVARC1000936, OVARC1000959, OVARC1000984, OVARC1001034, OVARC1001129, OVARC1001381, OVARC1001391, OVARC1001453, OVARC1001476, OVARC1001506, OVARC1001610, OVARC1001702, OVARC1001703, OVARC1001713, OVARC1001745, OVARC1001767, OVARC1002127, OVARC1002158, OVARC1002165, PLACE1000014, PLACE1000401,

【 0 8 2 0 】

PLACE1000562, PLACE1000611, PLACE1000656, PLACE1000712, PLACE1000909, PLACE1000948, PLACE1001241, PLACE1001257, PLACE1001377, PLACE1001517, PLACE1001610, PLACE1001771, PLACE1001817, PLACE1001983, PLACE1002213, PLACE1002395, PLACE1002500, PLACE1002714, PLACE1002722, PLACE1002794, PLACE1002851, PLACE1002908, PLACE1003045, PLACE1003238, PLACE1003296, PLACE1003369, PLACE1003493, PLACE1003537, PLACE1003553, PLACE1003768, PLACE1003771, PLACE1003903, PLACE1004197, PLACE1004258, PLACE1004270, PLACE1004289, PLACE1004473, PLACE1004743, PLACE1004840, PLACE1004969, PLACE1005086, PLACE1005206, PLACE1005313, PLACE1005530, PLACE1005595, PLACE1005623, PLACE1005763, PLACE1005884, PLACE1005934, PLACE1006225, PLACE1006754, PLACE1



006901, PLACE1006935, PLACE1006956, PLACE1007014, PLACE1007111, PLACE1007243, PLACE1007274, PLACE1007282, PLACE1007317, PLACE1007375, PLACE1007386, PLACE1007409, PLACE1007484, PLACE1007583, PLACE1007632, PLACE1007645, PLACE1007852, PLACE1007877, PLACE1008331, PLACE1008424, PLACE1008531, PLACE1008532, PLACE1008568, PLACE1008715, PLACE1009045, PLACE1009319, PLACE1009338, PLACE1009368, PLACE1009493, PLACE1009639, PLACE1009708, PLACE1009731, PLACE1010089, PLACE1010231, PLACE1010321, PLACE1010622, PLACE1010811, PLACE1010917, PLACE1010954, PLACE1011090, PLACE1011214, PLACE1011221, PLACE1011399, PLACE1011492, PLACE1011646, PLACE1011749, PLACE2000034, PLACE2000111, PLACE2000176,

【 0 8 2 1 】

PLACE2000187, PLACE2000341, PLACE2000379, PLACE2000425, PLACE2000458, PLACE3000020, PLACE3000218, PLACE3000226, PLACE3000244, PLACE3000413, PLACE4000052, PLACE4000129, PLACE4000300, PLACE4000387, PLACE4000581, PLACE4000593, PLACE4000650, THYRO1000394, THYRO1000395, THYRO1000570, THYRO1000748, THYRO1000756, THYRO1001134, THYRO1001271, THYRO1001401, THYRO1001534, THYRO1001541, THYRO1001809, Y79AA1000258, Y79AA1000420, Y79AA1000469, Y79AA1000734, Y79AA1000800, Y79AA1000976, Y79AA1001023, Y79AA1001177, Y79AA1001394, Y79AA1001603, Y79AA1001647, Y79AA1001846, Y79AA1001874, Y79AA1002139, Y79AA1002351, Y79AA1002399, Y79AA1002416

【 0 8 2 2 】

Pfamにより推定アミノ酸配列に機能ドメインを検出されたクローン名とヒットした機能ドメイン名は以下の通りであった。検索結果は、クローン名//機能ドメイン名のように示した。複数の機能ドメインがヒットした場合には//で区切って並記した。

HEMBA1000005//DnaJ, prokaryotic heat shock protein

HEMBA1000020//Tubulin

HEMBA1000129//Helicases conserved C-terminal domain

HEMBA1000156//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc finger, C2H2 type  
HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING finger)  
HEMBA1000411//Ank repeat  
HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)  
HEMBA1000531//Heat shock hsp70 proteins  
HEMBA1000561//Zinc finger, C2H2 type  
HEMBA1000608//Src homology domain 3  
HEMBA1000919//WD domain, G-beta repeats  
HEMBA1001043//Ank repeat  
HEMBA1001088//LIM domain containing proteins  
HEMBA1001137//Zinc finger, C2H2 type  
HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)  
HEMBA1001247//WW/rsp5/WWP domain containing proteins  
HEMBA1001286//Sushi domain  
HEMBA1001510//Basic region plus leucine zipper transcription factors  
HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)  
HEMBA1001661//Cadherin  
HEMBA1001723//WD domain, G-beta repeats  
HEMBA1001744//Eukaryotic protein kinase domain  
HEMBA1001804//Zinc finger, C2H2 type  
HEMBA1001819//Zinc finger, C2H2 type  
HEMBA1001847//Zinc finger, C2H2 type  
HEMBA1002035//Bromodomain  
HEMBA1002102//Ank repeat  
HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loop)

HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type

HEMBA1002212//Eukaryotic protein kinase domain

HEMBA1002215//LIM domain containing proteins

HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)

HEMBA1002768//Src homology domain 3

HEMBA1002810//WW/rsp5/WWP domain containing proteins

HEMBA1002818//EGF-like domain

HEMBA1002935//Zinc finger, C2H2 type

HEMBA1002939//Ank repeat

HEMBA1002973//3' 5'-cyclic nucleotide phosphodiesterases

HEMBA1003077//Fibronectin type III domain

HEMBA1003250//Eukaryotic protein kinase domain

HEMBA1003257//Zinc finger, C2H2 type

HEMBA1003281//IG superfamily

HEMBA1003291//Eukaryotic protein kinase domain

HEMBA1003433//Forkhead-associated (FHA) domain

HEMBA1003545//Homeobox domain //LIM domain containing proteins

HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1003684//Zinc finger, C2H2 type

HEMBA1003953//Zinc finger, C2H2 type

HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)

HEMBA1004227//Protein phosphatase 2C

HEMBA1004321//Zinc finger, C2H2 type

HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1004408//Peptidyl-prolyl cis-trans isomerases

HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)

HEMBA1004734//Ubiquitin-conjugating enzymes  
HEMBA1004973//Fibronectin type III domain  
HEMBA1005009//Actins  
HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
HEMBA1005581//EGF-like domain //Laminin G domain  
HEMBA1005732//Polyprenyl synthetases  
HEMBA1005737//EF hand  
HEMBA1006248//Zinc finger, C2H2 type  
HEMBA1006284//Ubiquitin family  
HEMBA1006293//IG superfamily  
HEMBA1006344//Band 4.1 family  
HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)  
HEMBA1006492//Ank repeat  
HEMBA1006559//Zinc finger, C3HC4 type (RING finger)  
HEMBA1006708//WD domain, G-beta repeats  
HEMBA1006737//Ank repeat  
HEMBA1006758//Cadherin  
HEMBA1006941//Thioredoxins  
HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases  
HEMBA1007300//3'5'-cyclic nucleotide phosphodiesterases  
HEMBA1000083//IG superfamily  
HEMBA1000317//EGF-like domain //Thrombospondin type 1 domain  
HEMBA1000556//Actinin-type actin-binding domain containing proteins //LI  
M domain containing proteins  
HEMBA1000725//Ras family (contains ATP/GTP binding P-loop)  
HEMBA1000781//Eukaryotic protein kinase domain  
HEMBA1000915//Thrombospondin type 1 domain  
HEMBA1000927//EF hand  
HEMBA1000947//Double-stranded RNA binding motif

HEMBB1001112//eubacterial secY protein  
HEMBB1001175//Ank repeat  
HEMBB1001234//WW/rsp5/WWP domain containing proteins  
HEMBB1001282//Ank repeat  
HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)  
HEMBB1001339//Forkhead-associated (FHA) domain  
HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type  
(RING finger)  
HEMBB1001802//Intermediate filament proteins  
HEMBB1001839//Zinc finger, C2H2 type  
HEMBB1002217//Zinc finger, C2H2 type  
HEMBB1002342//Thioredoxins  
HEMBB1002600//4 transmembrane segments integral membrane proteins  
MAMMA1000173//Src homology domain 3  
MAMMA1000388//Zinc finger, C2H2 type  
MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)  
MAMMA1000612//WD domain, G-beta repeats  
MAMMA1000672//Serine carboxypeptidases  
MAMMA1000731//SNF2 and others N-terminal domain  
MAMMA1001008//Eukaryotic aspartyl proteases  
MAMMA1001041//Actinin-type actin-binding domain containing proteins  
MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
MAMMA1001105//Zinc finger, C2H2 type  
MAMMA1001260//Zinc finger, C3HC4 type (RING finger)  
MAMMA1001576//Tubulin  
MAMMA1001735//Tubulin  
MAMMA1001768//ATPases associated with various cellular activities (AAA)  
MAMMA1001837//Zinc finger, C2H2 type

MAMMA1002170//Ribosomal protein S5  
MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2  
MAMMA1002637//Kinesin light chain repeat  
MAMMA1002650//Zinc finger, C2H2 type  
MAMMA1002671//AMP-binding enzymes  
MAMMA1002869//LIM domain containing proteins  
MAMMA1002881//SCP-like extracellular Proteins  
MAMMA1002937//Zinc finger, C2H2 type  
MAMMA1002938//Multicopper oxidases  
MAMMA1003011//Core histones H2A, H2B, H3 and H4  
MAMMA1003057//WD domain, G-beta repeats  
MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)  
NT2RM1000086//Zinc finger, C3HC4 type (RING finger)  
NT2RM1000199//CUB domain //Sushi domain  
NT2RM1000256//Glutamine amidotransferases class-II  
NT2RM1000499//Ank repeat  
NT2RM1000555//'Cold-shock' DNA-binding domain containing proteins  
NT2RM1000666//'Cold-shock' DNA-binding domain containing proteins //Zinc finger, CCHC, class  
NT2RM1000772//WD domain, G-beta repeats  
NT2RM1000826//'Cold-shock' DNA-binding domain containing proteins  
NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain  
NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases  
NT2RM1000885//Zinc finger, C3HC4 type (RING finger)  
NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)

NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C,  
 X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RM2000101//Zinc finger, C3HC4 type (RING finger)  
 NT2RM2000191//3' 5'-cyclic nucleotide phosphodiesterases  
 NT2RM2000422//Sodium:neurotransmitter symporter family  
 NT2RM2000490//C2 domain  
 NT2RM2000566//Integrins alpha chain  
 NT2RM2000577//tRNA synthetases class I  
 NT2RM2000594//C-5 cytosine-specific DNA methylases  
 NT2RM2000691//Actins  
 NT2RM2000735//Zinc finger, C2H2 type  
 NT2RM2000740//Helicases conserved C-terminal domain  
 NT2RM2000951//FGGY family of carbohydrate kinases  
 NT2RM2001324//LIM domain containing proteins  
 NT2RM2001499//Amino acid permeases  
 NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins  
 NT2RM2001613//eubacterial secY protein  
 NT2RM2001670//Zinc finger, C2H2 type  
 NT2RM2001700//Acyl-CoA dehydrogenases  
 NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RM2001813//WD domain, G-beta repeats  
 NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-  
 terminal domain  
 NT2RM2001896//Cytochrome C oxidase subunit II  
 NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RM2001997//Thioredoxins  
 NT2RM2002088//KH domain family of RNA binding proteins  
 NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-termin

al domain

NT2RM2002109//IG superfamily

NT2RM4000046//Zinc finger, C3HC4 type (RING finger)

NT2RM4000104//Zinc finger, C2H2 type

NT2RM4000167//Kinesin motor domain

NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-termin

al domain

NT2RM4000202//Zinc finger, C2H2 type

NT2RM4000229//PH (pleckstrin homology) domain

NT2RM4000344//ATPases associated with various cellular activities (AAA)

NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)

NT2RM4000471//Aminotransferases class-V

NT2RM4000496//ATPases associated with various cellular activities (AAA)

NT2RM4000611//WD domain, G-beta repeats

NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C,

Y domain

NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquiti  
n carboxyl-terminal hydrolases family 2

NT2RM4000733//Forkhead-associated (FHA) domain

NT2RM4000734//Zinc finger, C2H2 type

NT2RM4000751//Zinc finger, C2H2 type

NT2RM4000795//Carboxylesterases

NT2RM4000996//Zinc finger, C2H2 type

NT2RM4001054//eubacterial secY protein

NT2RM4001140//Homeobox domain

NT2RM4001178//DEAD and DEAH box helicases

NT2RM4001200//Zinc finger, C2H2 type

NT2RM4001313//Phosphatidylinositol 3- and 4-kinases

NT2RM4001316//Acyl-CoA dehydrogenases



NT2RM4001320//Src homology domain 3  
NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2  
NT2RM4001454//PH (pleckstrin homology) domain  
NT2RM4001483//Zinc finger, C2H2 type  
NT2RM4001629//Src homology domain 3  
NT2RM4001758//Eukaryotic protein kinase domain  
NT2RM4001810//Zinc finger, C2H2 type  
NT2RM4001813//Lectin C-type domain short and long forms  
NT2RM4001823//Zinc finger, C2H2 type  
NT2RM4001828//Zinc finger, C2H2 type  
NT2RM4001979//Zinc finger, C2H2 type  
NT2RM4001987//IG superfamily  
NT2RM4002013//WD domain, G-beta repeats  
NT2RM4002073//AMP-binding enzymes  
NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RM4002145//IG superfamily  
NT2RM4002287//Fibronectin type III domain  
NT2RM4002527//WD domain, G-beta repeats  
NT2RM4002623//tRNA synthetases class II  
NT2RP1000101//Zinc finger, C2H2 type  
NT2RP1000202//Ank repeat  
NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP1000363//PH (pleckstrin homology) domain  
NT2RP1000376//Ank repeat  
NT2RP1000470//DEAD and DEAH box helicases  
NT2RP1000478//Tubulin  
NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
NT2RP1000677//Kazal-type serine protease inhibitor domain

NT2RP1000701//WD domain, G-beta repeats  
NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
NT2RP1000782//4 transmembrane segments integral membrane proteins  
NT2RP1000833//3' 5'-cyclic nucleotide phosphodiesterases  
NT2RP1000856//4 transmembrane segments integral membrane proteins  
NT2RP1000947//Ubiquitin-conjugating enzymes  
NT2RP1000959//60s Acidic ribosomal protein  
NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP1001033//Tubulin  
NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
NT2RP1001177//Core histones H2A, H2B, H3 and H4  
NT2RP1001247//Transforming growth factor beta like domain  
NT2RP1001294//WD domain, G-beta repeats  
NT2RP1001302//WD domain, G-beta repeats  
NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases  
NT2RP1001457//WD domain, G-beta repeats  
NT2RP1001546//4 transmembrane segments integral membrane proteins  
NT2RP2000008//Zinc finger, C2H2 type  
NT2RP2000040//C2 domain  
NT2RP2000045//DnaJ, prokaryotic heat shock protein  
NT2RP2000054//Zinc finger, C3HC4 type (RING finger)  
NT2RP2000070//Cadherin  
NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain  
NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP2000224//PH (pleckstrin homology) domain  
NT2RP2000257//Mitochondrial carrier proteins

NT2RP2000329//Adenylate kinases  
NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP2000448//PH (pleckstrin homology) domain  
NT2RP2000660//ATPases associated with various cellular activities (AAA)  
NT2RP2000668//Eukaryotic protein kinase domain  
NT2RP2000710//tRNA synthetases class II  
NT2RP2000764//Aminotransferases class-V  
NT2RP2000842//7 transmembrane receptor (rhodopsin family)  
NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP2000932//Ank repeat  
NT2RP2001081//C2 domain  
NT2RP2001174//Zinc finger, C2H2 type  
NT2RP2001397//Cyclins  
NT2RP2001520//Mitochondrial carrier proteins  
NT2RP2001597//Zinc finger, C3HC4 type (RING finger)  
NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2  
NT2RP2001748//Polyprenyl synthetases  
NT2RP2001756//Zinc finger, C2H2 type  
NT2RP2001839//Eukaryotic protein kinase domain  
NT2RP2001900//Actins  
NT2RP2001991//Sodium:neurotransmitter symporter family  
NT2RP2002058//WD domain, G-beta repeats  
NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
NT2RP2002185//Ubiquitin family  
NT2RP2002208//Zinc finger, C3HC4 type (RING finger)  
NT2RP2002256//Cytochrome P450

NT2RP2002479//ABC transporters  
 NT2RP2002503//Zinc finger, C2H2 type  
 NT2RP2002520//Ank repeat  
 NT2RP2002591//Zinc finger, C2H2 type  
 NT2RP2002741//Src homology domain 3  
 NT2RP2002929//WD domain, G-beta repeats  
 NT2RP2002939//Zinc finger, C2H2 type  
 NT2RP2002959//Ubiquitin-conjugating enzymes  
 NT2RP2002980//Ribosomal protein S10  
 NT2RP2003137//Ubiquitin family  
 NT2RP2003164//Eukaryotic protein kinase domain  
 NT2RP2003228//MCM2/3/5 family  
 NT2RP2003243//Fibronectin type III domain  
 NT2RP2003272//Ubiquitin family  
 NT2RP2003307//Kinesin light chain repeat  
 NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP2003433//eubacterial secY protein  
 NT2RP2003480//Zinc finger, C2H2 type  
 NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP2003737//Ubiquitin-conjugating enzymes  
 NT2RP2003777//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2003840//Ubiquitin-conjugating enzymes  
 NT2RP2003857//Ank repeat  
 NT2RP2003981//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2004170//WD domain, G-beta repeats  
 NT2RP2004187//Zinc finger, C2H2 type  
 NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic protein kinase domain

NT2RP2004389//Ribosomal protein S9  
NT2RP2004538//PH (pleckstrin homology) domain  
NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
NT2RP2004710//WW/rsp5/WWP domain containing proteins  
NT2RP2004768//Eukaryotic protein kinase domain  
NT2RP2004933//Eukaryotic protein kinase domain  
NT2RP2004961//Zinc finger, C2H2 type  
NT2RP2005003//Zinc finger, C3HC4 type (RING finger)  
NT2RP2005012//DnaJ, prokaryotic heat shock protein  
NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
NT2RP2005139//Ank repeat  
NT2RP2005140//PH (pleckstrin homology) domain  
NT2RP2005239//Aminotransferases class-V  
NT2RP2005288//Regulator of chromosome condensation (RCC1)  
NT2RP2005293//PH (pleckstrin homology) domain  
NT2RP2005325//Homeobox domain //LIM domain containing proteins  
NT2RP2005344//E1-E2 ATPases  
NT2RP2005465//Mitochondrial carrier proteins  
NT2RP2005525//Forkhead-associated (FHA) domain  
NT2RP2005531//Band 4.1 family  
NT2RP2005557//Bacterial mutT protein  
NT2RP2005654//DnaJ, prokaryotic heat shock protein  
NT2RP2005701//Zinc finger, C3HC4 type (RING finger)  
NT2RP2005722//Zinc finger, C2H2 type  
NT2RP2005752//TNFR/NGFR cysteine-rich region  
NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain

NT2RP2005767//HMG (high mobility group) box  
NT2RP2006312//HMG (high mobility group) box  
NT2RP2006464//HMG (high mobility group) box  
NT2RP2006571//Cytochrome P450  
NT2RP3000050//Zinc finger, C2H2 type  
NT2RP3000068//PH (pleckstrin homology) domain  
NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (C  
PSase)  
NT2RP3000299//Src homology domain 3  
NT2RP3000359//Adenylate kinases  
NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)  
NT2RP3000403//WW/rsp5/WWP domain containing proteins  
NT2RP3000487//WW/rsp5/WWP domain containing proteins  
NT2RP3000512//Homeobox domain  
NT2RP3000527//Zinc finger, C2H2 type  
NT2RP3000531//IG superfamily  
NT2RP3000590//Zinc finger, C3HC4 type (RING finger)  
NT2RP3000603//Helix-loop-helix DNA-binding domain  
NT2RP3000605//Zinc finger, C2H2 type  
NT2RP3000632//Zinc finger, C2H2 type  
NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //  
Phosphatidylinositol-specific phospholipase C, Y domain  
NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP bi  
nding P-loop)  
NT2RP3000825//EGF-like domain  
NT2RP3000869//ATPases associated with various cellular activities (AAA)  
NT2RP3000994//Double-stranded RNA binding motif  
NT2RP3001057//Zinc finger, C2H2 type  
NT2RP3001084//PH (pleckstrin homology) domain

NT2RP3001120//Zinc finger, C2H2 type  
NT2RP3001140//Thrombospondin type 1 domain  
NT2RP3001150//Forkhead-associated (FHA) domain  
NT2RP3001155//HMG (high mobility group) box  
NT2RP3001214//Zinc finger, C2H2 type  
NT2RP3001268//Zinc finger, C2H2 type  
NT2RP3001338//Zinc finger, C2H2 type  
NT2RP3001355//Mitochondrial carrier proteins  
NT2RP3001398//Zinc finger, C2H2 type  
NT2RP3001426//DnaJ, prokaryotic heat shock protein  
NT2RP3001453//ABC transporters  
NT2RP3001457//PH (pleckstrin homology) domain  
NT2RP3001472//HMG (high mobility group) box  
NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/W  
WP domain containing proteins  
NT2RP3001497//Zinc finger, C3HC4 type (RING finger)  
NT2RP3001724//Helicases conserved C-terminal domain  
NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP3001943//Zinc finger, C3HC4 type (RING finger)  
NT2RP3001944//Zinc finger, C3HC4 type (RING finger)  
NT2RP3002007//ATPases associated with various cellular activities (AAA)  
NT2RP3002054//Low-density lipoprotein receptor domain class A  
NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
NT2RP3002399//MCM2/3/5 family  
NT2RP3002501//Serine/threonine dehydratases  
NT2RP3002602//Thioredoxins  
NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins  
NT2RP3002663//PH (pleckstrin homology) domain

NT2RP3002909//Ank repeat  
NT2RP3002953//Cadherin  
NT2RP3002969//AMP-binding enzymes  
NT2RP3003061//Ank repeat  
NT2RP3003145//Zinc carboxypeptidases  
NT2RP3003230//WD domain, G-beta repeats  
NT2RP3003251//Zinc finger, C3HC4 type (RING finger)  
NT2RP3003278//Ank repeat //Zinc finger, C2H2 type  
NT2RP3003282//PH (pleckstrin homology) domain  
NT2RP3003311//PH (pleckstrin homology) domain  
NT2RP3003385//Ank repeat //Chaperonins clpA/B  
NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)  
NT2RP3003621//CUB domain //Kringle domain  
NT2RP3003701//Thrombospondin type 1 domain  
NT2RP3003716//Fibronectin type III domain  
NT2RP3003809//ATPases associated with various cellular activities (AAA)  
NT2RP3004016//Zinc finger, C3HC4 type (RING finger)  
NT2RP3004207//CUB domain //Sushi domain  
NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
NT2RP3004242//PH (pleckstrin homology) domain  
NT2RP3004262//DnaJ, prokaryotic heat shock protein  
NT2RP3004566//Zinc finger, C2H2 type  
NT2RP3004569//Ank repeat  
NT2RP3004594//HMG (high mobility group) box  
NT2RP3004617//Zinc finger, C3HC4 type (RING finger)  
NT2RP4000259//Glutathione peroxidases  
NT2RP4000370//Prokaryotic-type class I peptide chain release factors  
NT2RP4000376//WD domain, G-beta repeats



NT2RP4000398//Zinc finger, C2H2 type  
NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type  
(RING finger)  
NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2  
NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-termin  
al domain  
NT2RP4000588//Actinin-type actin-binding domain containing proteins  
NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type  
(RING finger)  
NT2RP4000837//Zinc finger, C2H2 type  
NT2RP4000839//WD domain, G-beta repeats  
NT2RP4000865//Zinc finger, C2H2 type  
NT2RP4000907//Fibronectin type III domain //IG superfamily  
NT2RP4000925//Fibronectin type III domain  
NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquiti  
n carboxyl-terminal hydrolases family 2  
NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins  
NT2RP4001079//E1-E2 ATPases  
NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
NT2RP4001117//eubacterial secY protein  
NT2RP4001150//Fibronectin type III domain  
NT2RP4001213//Zinc finger, C2H2 type  
NT2RP4001219//Thioredoxins  
NT2RP4001235//Zinc finger, CCHC class  
NT2RP4001433//Zinc finger, C2H2 type  
NT2RP4001498//Ank repeat  
NT2RP4001568//Ank repeat  
NT2RP4001644//Eukaryotic protein kinase domain

NT2RP4001725//WD domain, G-beta repeats  
NT2RP4001753//Zinc finger, C2H2 type  
NT2RP4001790//Zinc finger, C2H2 type  
NT2RP4001822//4 transmembrane segments integral membrane proteins  
NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain  
in  
NT2RP4001893//Ank repeat  
NT2RP4001896//WD domain, G-beta repeats  
NT2RP4001927//WD domain, G-beta repeats  
NT2RP4001938//Zinc finger, C2H2 type  
NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
NT2RP4002078//Zinc finger, C2H2 type  
NT2RP4002408//Eukaryotic protein kinase domain  
NT2RP4002905//Cyclins  
NT2RP5003477//WD domain, G-beta repeats  
OVARC1000006//Core histones H2A, H2B, H3 and H4  
OVARC1000085//Proteasome A-type and B-type  
OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
OVARC1000556//Eukaryotic protein kinase domain  
OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2  
OVARC1000746//Double-stranded RNA binding motif  
OVARC1000885//Alcohol/other dehydrogenases, short chain type  
OVARC1000937//Cyclins  
OVARC1000999//Ank repeat  
OVARC1001154//Granulins  
OVARC1001180//Ubiquitin family  
OVARC1001306//Helix-loop-helix DNA-binding domain  
OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)

OVARC1001731//Tropomyosins  
OVARC1001943//Zinc finger, C2H2 type  
OVARC1002050//Spectrin alpha chain, repeated domain  
OVARC1002112//Core histones H2A, H2B, H3 and H4  
OVARC1002138//ATPases associated with various cellular activities (AAA)  
OVARC1002182//WD domain, G-beta repeats  
PLACE1000014//Zinc finger, C3HC4 type (RING finger)  
PLACE1000040//Ras family (contains ATP/GTP binding P-loop)  
PLACE1000050//Zinc finger, C2H2 type  
PLACE1000081//PH (pleckstrin homology) domain  
PLACE1000142//Enoyl-CoA hydratase/isomerase  
PLACE1000401//IG superfamily  
PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
PLACE1000420//Bacterial mutT protein  
PLACE1000706//Bromodomain  
PLACE1000769//KH domain family of RNA binding proteins  
PLACE1000786//PH (pleckstrin homology) domain  
PLACE1000863//Ribosomal protein S4  
PLACE1000909//Ank repeat  
PLACE1000972//Src homology domain 3  
PLACE1000979//Zinc finger, C2H2 type  
PLACE1001304//Zinc finger, C2H2 type  
PLACE1001387//Src homology domain 3  
PLACE1001632//Zinc finger, C2H2 type  
PLACE1001672//Aminotransferases class-III pyridoxal-phosphate  
PLACE1001716//Zinc finger, CCHC class  
PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
PLACE1001781//Phosphoglucomutase and phosphomannomutase phosphoserine

PLACE1001869//FGGY family of carbohydrate kinases  
PLACE1002438//Zinc finger, C2H2 type  
PLACE1002450//Zinc finger, C2H2 type  
PLACE1002474//EGF-like domain //von Willebrand factor type A domain  
PLACE1002499//Zinc finger, C3HC4 type (RING finger)  
PLACE1002532//Homeobox domain  
PLACE1002571//Actins  
PLACE1002685//Src homology domain 2  
PLACE1002722//7 transmembrane receptor (rhodopsin family)  
PLACE1002775//Bromodomain  
PLACE1002834//Zinc finger, C2H2 type  
PLACE1003100//Alcohol/other dehydrogenases, short chain type  
PLACE1003174//Ubiquitin-conjugating enzymes  
PLACE1003238//7 transmembrane receptor (rhodopsin family)  
PLACE1003302//Zinc finger, C2H2 type  
PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
PLACE1003366//C2 domain  
PLACE1003394//Ras family (contains ATP/GTP binding P-loop)  
PLACE1003420//Mitochondrial carrier proteins  
PLACE1003493//C1q domain  
PLACE1003519//KH domain family of RNA binding proteins  
PLACE1003723//Src homology domain 2  
PLACE1003738//Zinc finger, C2H2 type  
PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C,  
X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
PLACE1004128//WD domain, G-beta repeats  
PLACE1004358//PH (pleckstrin homology) domain  
PLACE1004428//Acyl-CoA dehydrogenases  
PLACE1004437//Isocitrate and isopropylmalate dehydrogenases

PLACE1004506//LIM domain containing proteins  
PLACE1004674//EF hand  
PLACE1004918//L-lactate dehydrogenases  
PLACE1005243//Eukaryotic protein kinase domain  
PLACE1005305//Adenylate kinases  
PLACE1005327//Src homology domain 3  
PLACE1005530//Zinc finger, C3HC4 type (RING finger)  
PLACE1005646//Helicases conserved C-terminal domain  
PLACE1005656//Ribonucleotide reductases  
PLACE1005966//WD domain, G-beta repeats  
PLACE1006157//Sushi domain  
PLACE1006196//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
PLACE1006438//Zinc finger, C2H2 type  
PLACE1006626//Double-stranded RNA binding motif  
PLACE1006754//IG superfamily  
PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
PLACE1006956//ABC transporters  
PLACE1006958//Heat shock hsp70 proteins  
PLACE1007375//C2 domain  
PLACE1007488//PH (pleckstrin homology) domain  
PLACE1007511//Intermediate filament proteins  
PLACE1007537//Ank repeat  
PLACE1007544//Zinc finger, C2H2 type  
PLACE1007547//Zinc finger, C3HC4 type (RING finger)  
PLACE1007598//Zinc finger, C2H2 type  
PLACE1007697//ABC transporters

PLACE1007958//3' 5'-cyclic nucleotide phosphodiesterases  
PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
PLACE1008201//Zinc finger, C2H2 type  
PLACE1008429//Ank repeat  
PLACE1008465//Zinc finger, C2H2 type  
PLACE1008650//WD domain, G-beta repeats  
PLACE1009020//Aminotransferases class-V  
PLACE1009094//von Willebrand factor type C domain  
PLACE1009099//Zinc finger, C2H2 type  
PLACE1009246//LIM domain containing proteins  
PLACE1009468//WD domain, G-beta repeats  
PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
PLACE1009524//PH (pleckstrin homology) domain  
PLACE1009596//WD domain, G-beta repeats  
PLACE1009622//Double-stranded RNA binding motif  
PLACE1009861//Cysteine proteases  
PLACE1009925//Helicases conserved C-terminal domain  
PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin  
PLACE1010053//Double-stranded RNA binding motif  
PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2  
PLACE1010702//Zinc finger, C2H2 type  
PLACE1010833//EF hand  
PLACE1010926//Src homology domain 3  
PLACE1010960//Actins  
PLACE1011041//Src homology domain 3  
PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
PLACE1011114//Helicases conserved C-terminal domain

PLACE1011160//Zinc finger, C3HC4 type (RING finger)  
PLACE1011263//Ank repeat  
PLACE1011433//Zinc finger, C2H2 type  
PLACE1011576//Zinc finger, C2H2 type  
PLACE1011923//Eukaryotic protein kinase domain  
PLACE2000034//Fibronectin type III domain //IG superfamily  
PLACE2000072//Zinc finger, C2H2 type  
PLACE2000111//IG superfamily  
PLACE2000164//WD domain, G-beta repeats  
PLACE2000216//PH (pleckstrin homology) domain  
PLACE2000341//Sodium:solute symporter family  
PLACE2000371//Src homology domain 2  
PLACE2000373//Thrombospondin type 1 domain  
PLACE2000398//IG superfamily  
PLACE2000427//Helicases conserved C-terminal domain  
PLACE2000458//Cadherin  
PLACE3000020//Guanylate cyclases  
PLACE3000169//Zinc finger, C2H2 type  
PLACE4000014//Helicases conserved C-terminal domain  
PLACE4000052//ABC transporters  
PLACE4000192//Zinc finger, C2H2 type  
PLACE4000211//Bromodomain  
PLACE4000431//Helicases conserved C-terminal domain  
PLACE4000522//Ank repeat  
PLACE4000581//EGF-like domain //Sushi domain  
PLACE4000654//Ubiquitin-conjugating enzymes  
THYRO1000072//IG superfamily  
THYRO1000242//Zinc finger, C2H2 type  
THYRO1000288//Zinc-binding metalloprotease domain

THYRO1000488//Zinc finger, C3HC4 type (RING finger)  
THYRO1000501//Zinc finger, C3HC4 type (RING finger)  
THYRO1000666//Kinesin motor domain  
THYRO1000748//Src homology domain 3  
THYRO1000926//3'5'-cyclic nucleotide phosphodiesterases  
THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
THYRO1001671//Ubiquitin family  
Y79AA1000037//Zinc finger, C3HC4 type (RING finger)  
Y79AA1000214//Core histones H2A, H2B, H3 and H4  
Y79AA1000342//Zinc finger, C2H2 type  
Y79AA1000349//Double-stranded RNA binding motif  
Y79AA1000627//Zinc finger, C2H2 type  
Y79AA1000705//Helicases conserved C-terminal domain  
Y79AA1000752//KH domain family of RNA binding proteins  
Y79AA1000833//Tubulin  
Y79AA1001048//Acyl-CoA dehydrogenases  
Y79AA1001391//Homeobox domain  
Y79AA1001394//ATPases associated with various cellular activities (AAA)  
Y79AA1001493//Ubiquitin-conjugating enzymes  
Y79AA1001613//Zinc finger, C2H2 type  
Y79AA1001874//TNFR/NGFR cysteine-rich region  
Y79AA1002027//Ubiquitin-conjugating enzymes  
Y79AA1002139//DnaJ, prokaryotic heat shock protein  
Y79AA1002208//Ank repeat  
Y79AA1002246//C2 domain  
Y79AA1002307//Fibronectin type III domain  
Y79AA1002472//Zinc finger, C2H2 type

【 0 8 2 3 】

【発明の効果】



本発明により、5601にも及ぶ新規な全長cDNAと、このcDNAを合成することができるプライマーが提供された。全長cDNAの分離が進んでいないヒトにおいて、新規な全長cDNAを提供した意義は大きい。本発明のcDNAは全長であるため、翻訳開始点を含み、タンパク質の機能解析において有用な情報を与える。

これらのcDNAは、分泌タンパク質、膜タンパク質、シグナル伝達関連タンパク質、Glycoprotein関連タンパク質、転写関連タンパク質などを含む生体において重要な機能を持つタンパク質をコードしていることが考えられ、また、多くの疾患に関連していることが予想される。疾患に関連した遺伝子やタンパク質は、診断マーカー、発現や活性を制御する医薬品の開発、あるいは遺伝子治療のターゲットになるなど医薬品の開発等に有効である。

【0824】

相同性検索結果データ1.

5'末端クローン配列に対するSwissProt相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのOrganism、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

ここでP値とは、配列間の類似性を統計的に起こりうる確率を考慮してスコアで示したもので、一般に値が小さいと類似性が高い(Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272)。

F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712

F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T

RNA LIGASE) (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996  
 F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULA  
 TA (HISTOPLASMA CAPSULATUM).//P41742  
 F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//  
 PLASMODIUM KNOWLESI (STRAIN NURI).//P04922  
 F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS E  
 DULIS (BLUE MUSSEL).//P80247  
 F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P  
 80355  
 F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86  
 :41:41//HOMO SAPIENS (HUMAN).//P56385  
 F-HEMBA1000111  
 F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE  
 T4.//P20703  
 F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAK  
 ER'S YEAST).//P38374  
 F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.4e-16:47:70/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SA  
 IMIRI (STRAIN 11).//Q01042  
 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:4  
 0//HOMO SAPIENS (HUMAN).//Q93074  
 F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:  
 36//MUS MUSCULUS (MOUSE).//P81122  
 F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMM  
 UNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286  
 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P221

F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814

F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS (MOUSE).//P05142

F-HEMBA1000213

F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P4048

0

F-HEMBA1000251

F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552

F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED COBRA) (NAJA NAJA SIAMENSIS).//P14613

F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.14:26:65//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000288

F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO SAPIENS (HUMAN).//P10516

F-HEMBA1000302

F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//CAENORHABDITIS ELEGANS.//Q03601

F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.021:18:83//H  
OMO SAPIENS (HUMAN).//P39194

F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235:2  
5//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922

F-HEMBA1000327

F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FI  
SSION YEAST).//Q10193

F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.8e-26:36:83/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000351

F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.99:22:50//HOMO  
SAPIENS (HUMAN).//P02811

F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES  
VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-35:105:74  
//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:4  
2//ARCHAEOGLOBUS FULGIDUS.//028646

F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//  
HOMO SAPIENS (HUMAN).//P78352

F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//6.8e-08:66:42//MUS MUSCULUS (  
MOUSE).//P11369

F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1  
.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P209  
62

F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-30:92:69/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000411

F-HEMBA1000418

F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.3e-10:90:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000434

F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87048

F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT).//P33279

F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHAGE ALPHA-3.//P31280

F-HEMBA1000464

F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P43502

F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38//HOMO SAPIENS (HUMAN).//Q13105

F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427

F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVEGICUS (RAT).//P97538

F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-20:81:54//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000504

F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32/  
/HOMO SAPIENS (HUMAN).//Q02410

F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCO  
SAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S  
YEAST).//P29465

F-HEMBA1000518

F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-37:68:75/  
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.2e-09:75:49/  
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSC  
ULUS (MOUSE).//Q01755

F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBI  
MANUS (NEW WORLD MALARIA MOSQUITO).//P41827

F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.7e-32:96:78/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.  
0:12:75//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36  
499

F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089  
:79:31//MUS MUSCULUS (MOUSE).//P15265

F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SAC  
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730

F-HEMBA1000557

F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1e-18:200:28//HOMO  
SAPIENS (HUMAN).//P51508

F-HEMBA1000563

F-HEMBA1000568

F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS  
(HUMAN).//Q14444

F-HEMBA1000575

F-HEMBA1000588

F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-17:41:92/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HO  
MO SAPIENS (HUMAN).//Q02224

F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III./  
/0.93:24:54//CAENORHABDITIS ELEGANS.//P41997

F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00010:49:55//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:6  
1//HOMO SAPIENS (HUMAN).//043295

F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-21:94:62//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36  
//VOLVOX CARTERI.//P21997

F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAP  
IENS (HUMAN).//P04281

F-HEMBA1000655

F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P35197

F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRIS  
EUS (CHINESE HAMSTER).//P02799

F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.1e-17:86:59/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] ./3.0e-13:45:44//MUS MUSCULUS (MOUSE) ./P11369

F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4.5e-07:79:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) ./013873

F-HEMBA1000702

F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE) ./Q02722

F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CASTELLANII (AMOEBA) ./P10569

F-HEMBA1000722

F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.4e-32:83:77//HOMO SAPIENS (HUMAN) ./P39191

F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN) ./0.73:26:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) ./P47977

F-HEMBA1000747

F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44211

F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO SAPIENS (HUMAN) ./P10267

F-HEMBA1000769

F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUMAN) ./043316

F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.3e-23:92:63//HOMO SAPIENS (HUMAN) ./P39188

F-HEMBA1000791

F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R) ./0.079:87:29//CERVUS ELAPHUS (RED DEER) ./Q28235

F-HEMBA1000822

F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS



(STRAIN COPENHAGEN).//P20546  
 F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//  
 0.92:46:34//CAENORHABDITIS ELEGANS.//P41953  
 F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC  
 HOMEBOX PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951  
 F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:2  
 9:100//HOMO SAPIENS (HUMAN).//P51689  
 F-HEMBA1000867  
 F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS T  
 YPE 18.//P06792  
 F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALU  
 S DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333  
 F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FI  
 SSION YEAST).//P41891  
 F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745  
 F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.69:43:37//HOMO SAPIENS (HUMAN).//P30808  
 F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-  
 08:44:38//HOMO SAPIENS (HUMAN).//O15480  
 F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:5  
 2//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P22667  
 F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR  
 -A/PFR-B).//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225  
 F-HEMBA1000934  
 F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.85:27:59//HOM  
 O SAPIENS (HUMAN).//P39188  
 F-HEMBA1000943  
 F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19  
 958

F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.0097:29:72//  
HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND  
MT-20-IIIB).//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL).//P80253

F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR  
VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1000972

F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA GENI  
TALIUM.//P47679

F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRA  
GMENT).//0.028:57:36//HOMO SAPIENS (HUMAN).//P25067

F-HEMBA1000985

F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECUR  
SOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:34//RATTUS  
NORVEGICUS (RAT).//P08462

F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN  
D2013.2 IN CHROMOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q1896  
4

F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS  
(HUMAN).//Q14684

F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.4e-25:61:70/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS ELEG  
ANS.//P34687

F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-8  
5:191:84//RATTUS NORVEGICUS (RAT).//P33671

F-HEMBA1001019

F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.7e-24:49:73//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001022

F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//051100

F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).//P24712

F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES HYGROSCOPICUS.//P16961

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4) (N- ACETYL GALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFATASE) (GALNAC6S SULFATASE) (CHONDROITINSULFATASE) (CHONDROITINASE).//3.2e-132:249:94//HOMO SAPIENS (HUMAN).//P34059

F-HEMBA1001060

F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:96//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//HOMO SAPIENS (HUMAN).//043918

F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP 34.5).//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319

F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP 5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULUS (MOUSE).//Q60676

F-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5e-50:176:57//HOMO SAPIENS (HUMAN).//P48059

F-HEMBA1001094

F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EH A-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:60//ECTOTHIORHODOSPIRA HALOPHILA.//P80101

F-HEMBA1001109//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.7e-37:102:82 //HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001122

F-HEMBA1001123

F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV).//P19033

F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e-22:103:52//HOMO SAPIENS (HUMAN).//P51523

F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO SAPIENS (HUMAN).//P53420

F-HEMBA1001172

F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:79//RATTUS NORVEGICUS (RAT).//P51646

F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35 C) (FRAGMENT).//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (BARBARY APE).//Q95145

F-HEMBA1001208

F-HEMBA1001213

F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.99.46) (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91//HOMO SAPIENS (HUMAN).//P25788

F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28749

F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00052:16  
:81//VOLVOX CARTERI.//P21997

F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.).//1.6e-68:178  
:77//RATTUS NORVEGICUS (RAT).//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.7  
8) (BETA- MANNANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A).//0.67:23:  
60//PIROMYCES SP.//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76).//0.83:48:35//  
PORPHYRA PURPUREA.//P51229

F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//1.3e-07  
:185:29//CAVIA PORCELLUS (GUINEA PIG).//Q60401

F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.//0.00018:15  
9:30//RATTUS NORVEGICUS (RAT).//P31422

F-HEMBA1001294

F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.3e-07:27:77/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DE  
RIVED FACTOR 4) (SDF-4).//3.3e-61:150:76//MUS MUSCULUS (MOUSE).//Q61112

F-HEMBA1001303

F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161.//2.7e-10:170:27//HOMO SAP  
IENS (HUMAN).//P50876

F-HEMBA1001319

F-HEMBA1001323

F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REG  
ION.//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601

F-HEMBA1001327

F-HEMBA1001330

F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDIN  
G PROTEIN (VAP-33).//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA

HARE).//Q16943

F-HEMBA1001361//RUBREDOXIN (RD).//0.95:44:29//ALCALIGENES EUTROPHUS.//P3  
1912

F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN.//0.013:45:33//AEROMONAS SO  
BRIA.//P09165

F-HEMBA1001377//SPERM PROTAMINE P1.//1.0:22:40//PLANIGALE MACULATA SINUA  
LIS (COMMON PLANIGALE).//018746

F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.60:  
37:29//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).  
//P12506

F-HEMBA1001387//GTP-BINDING PROTEIN TC10.//6.6e-43:83:92//HOMO SAPIENS (  
HUMAN).//P17081

F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).//0.00088:46:45  
//HOMO SAPIENS (HUMAN).//Q14149

F-HEMBA1001391

F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE).//1.0:59:37//ESCHERI  
CHIA COLI.//P00645

F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.2  
5:41:34//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4  
AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.0e-09:129:40//  
HOMO SAPIENS (HUMAN).//P04280

F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGI  
ON (0313).//0.95:88:31//ESCHERICHIA COLI.//P55140

F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT).//0.95:46:32//MUS MUSCULUS (MO  
USE).//Q04890

F-HEMBA1001415//HISTONE H5.//0.43:95:29//GALLUS GALLUS (CHICKEN).//P0225  
9

F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR.//0.77:46:32//LACTOCOCCUS

LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068  
 F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.8e-09:132:31//N  
 YCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-31:84:77/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBA1001442  
 F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.71:41:39//PSEUDOPLEUR  
 ONECTA AMERICANUS (WINTER FLOUNDER).//P02734  
 F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17.//0.13:127:27//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//Q12446  
 F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.57:38:47/  
 /HANSENULA WINGEI (YEAST).//P48882  
 F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-).//0.98:124:25//BORR  
 ELIA BURGDORFERI (LYME DISEASE SPIROCHÈTE).//Q44737  
 F-HEMBA1001463//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-32:62:67/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159).//6.8e-  
 09:252:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40477  
 F-HEMBA1001478  
 F-HEMBA1001497//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-33:105:72  
 //HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1001510//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.3e-37:54:81/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-63:223:57//H  
 OMO SAPIENS (HUMAN).//P08547  
 F-HEMBA1001517  
 F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//CO  
 TURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P49437  
 F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:

130:29//CLOSTRIDIUM PASTEURIANUM.//P29166  
 F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS  
 TYPE 6A.//Q84296  
 F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//1.5e-07:  
 99:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898  
 F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGD  
 ORFERI (LYME DISEASE SPIROCHETE).//051635  
 F-HEMBA1001569//SYNAPTOSOMAL 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2)  
 (VAMP-2).//2.2e-50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE)  
 .//P19065  
 F-HEMBA1001570//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.3e-33:107:72  
 //HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-HEMBA1001581  
 F-HEMBA1001585  
 F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33/  
 /HUMAN ADENOVIRUS TYPE 2.//P03263  
 F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPI  
 ENS (HUMAN).//Q14141  
 F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOX  
 YLATE COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q286  
 15  
 F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4  
 .3e-45:222:46//SPIRODELA POLYRRHIZA.//P42803  
 F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q2205  
 3  
 F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//H  
 OMO SAPIENS (HUMAN).//Q09155



F-HEMBA1001640//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-06:80:41//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS  
(HUMAN).//000268

F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO SAPIENS (HUMAN).//Q0837  
9

F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES C  
EREVISIAE (BAKER'S YEAST).//Q12446

F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD SUBUNI  
T (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN--COENZYME M METHYLTRAN  
SFERASE 12 KD SUBUNIT).//1.0:29:44//METHANOBACTERIUM THERMOAUTOTROPHICUM  
(STRAIN MARBURG / DSM 2133).//Q50773

F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTE  
R XYLINUM (ACETOBACTER PASTEURIANUS).//P37697

F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:35  
//PLASMODIUM CYNOMOLGI (STRAIN BEROK).//P08672

F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX (S  
OYBEAN).//P08960

F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.2e-13:62:64/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REG  
ION (P40) (ORF3) (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID  
POLYHEDROSIS VIRUS (OPMNPV).//P24653

F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:5  
4:37//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REG  
ION.//0.59:109:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042

F-HEMBA1001711

F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0.54:44:34//HUMAN ADENOVIRUS TYPE 41.//P23690

F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:75//RATTUS NORVEGICUS (RAT).//Q03344

F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16820

F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318

F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV).//P25221

F-HEMBA1001734

F-HEMBA1001744//SCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116

F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTERIUM LEPRAE.//P38388

F-HEMBA1001761

F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40//HOMO SAPIENS (HUMAN).//P17023

F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46//CAENORHABDITIS ELEGANS.//Q11116

F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216

F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:48//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1001803

F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//  
 9.3e-17:56:57//ORYZA SATIVA (RICE).//P25074

F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU  
 -ANTIGEN D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//009032

F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORA  
 BIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:  
 30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P05733

F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS  
 (HUMAN).//P52742

F-HEMBA1001820

F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15  
 (PROTEIN EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567

F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
 //4.7e-11:124:37//OVIS ARIES (SHEEP).//P26372

F-HEMBA1001835

F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-14:36:63/  
 /HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MU  
 SCULUS (MOUSE).//Q07230

F-HEMBA1001861

F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-  
 IB) (ST-H).//1.0:31:38//ESCHERICHIA COLI.//P07965

F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (   
 EC 2.4.1.-) (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT FLY)  
 .//Q09332

F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I.  
 //5.3e-13:65:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362

F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:37//STREPT

OMYCES FRADIAE.//P26800  
 F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (M  
 E2GLYDH).//9.8e-20:250:29//RATTUS NORVEGICUS (RAT).//Q63342  
 F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EI  
 F4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAE  
 NORHABDITIS ELEGANS.//O61955  
 F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-07:53:62//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE  
 (BAKER' S YEAST).//P43535  
 F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA C  
 OLI.//Q52280  
 F-HEMBA1001918  
 F-HEMBA1001921  
 F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONT  
 ELLA SINENSIS.//P49560  
 F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0017:31:77//H  
 OMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (H  
 IBERNATOR- SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS AS  
 IATICUS (CHIPMUNK).//Q06577  
 F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGIO  
 N (ORF E).//1.0:35:37//BACTERIOPHAGE T4.//P32269  
 F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44/  
 /DROSOPHILA YAKUBA (FRUIT FLY).//P03933  
 F-HEMBA1001960//HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HO  
 MO SAPIENS (HUMAN).//Q00444  
 F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5' REGION.//1.0:30:36  
 //SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P53056

F-HEMBA1001964

F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGA  
LOVIRUS (STRAIN AD169).//P16818

F-HEMBA1001979

F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGYI  
A PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010356

F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I).//0.99:31:45//ANEMONIA SULCAT  
A (SNAKE-LOCKS SEA ANEMONE).//P01533

F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFI  
C (EC 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467

F-HEMBA1002008

F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSI  
S THALIANA (MOUSE-EAR CRESS).//Q42377

F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH)./  
/P12704

F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//  
HOMO SAPIENS (HUMAN).//Q92794

F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:4  
0//HOMO SAPIENS (HUMAN).//Q92558

F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:37:75//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002084

F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE (B  
AKER'S YEAST).//P35210

F-HEMBA1002100

F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357

F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICA  
GO TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOP

HILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].  
 //0.35:111:33//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338  
 F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC RE  
 GION.//0.88:72:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192  
 F-HEMBA1002144  
 F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:6  
 5:46//BOS TAURUS (BOVINE).//P06579  
 F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:28/  
 /SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .93:58:25//APIS MELLIFERA (HONEYBEE).//P34859  
 F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.1e-21:94:65/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-5  
 1:180:56//SUS SCROFA (PIG).//P79293  
 F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.1e-40:102:75  
 //HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-13:133:45/  
 /HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153  
 :26//HOMO SAPIENS (HUMAN).//P52746  
 F-HEMBA1002185  
 F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.86:46:45//HO  
 MO SAPIENS (HUMAN).//P39194  
 F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:57//DROSO  
 PHILA MELANOGASTER (FRUIT FLY).//Q01644  
 F-HEMBA1002199  
 F-HEMBA1002204

F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE  
 DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:30//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q24324

F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:14  
 7:84//MUS MUSCULUS (MOUSE).//P47226

F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.6e-26:168:44/  
 /HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//6.8e-18:68:72  
 //HOMO SAPIENS (HUMAN).//P39190

F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA ACER  
 VULINA.//P21959

F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS  
 (COMMON SEA URCHIN).//P80367

F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AU  
 RATUS (GOLDEN HAMSTER).//P17808

F-HEMBA1002257

F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01644

F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS  
 GALLUS (CHICKEN).//Q90667

F-HEMBA1002270

F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:40//BA  
 CTERIOPHAGE PHI-105.//P10437

F-HEMBA1002328

F-HEMBA1002337

F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//M  
 US MUSCULUS (MOUSE).//Q62415

F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS T  
 YPE 35.//P27226

F-HEMBA1002349

F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:71//XE  
NOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-24:69:73//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAG  
O TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)./  
/2.6e-51:187:56//MUS MUSCULUS (MOUSE).//P39447

F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMA  
N).//P02814

F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REG  
ION.//0.042:41:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:  
47:29//CALYPTROSPHAERA SPHAEROIDEA.//P41548

F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:1  
09:55//HOMO SAPIENS (HUMAN).//Q00994

F-HEMBA1002460

F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:  
80:30//HOMO SAPIENS (HUMAN).//P81489

F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO S  
APIENS (HUMAN).//P52756

F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS  
MUSCULUS (MOUSE).//P05143

F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-34:96:71/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1002486

F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39  
//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P48732



F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKE  
R' S YEAST).//P38166

F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.0e-06:49:63//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-22:169:44  
//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV./  
/0.00017:79:35//CAENORHABDITIS ELEGANS.//Q20296

F-HEMBA1002515

F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//1.0:  
53:37//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P81449

F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.7e-32:96:75//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002547//AGRIN PRECURSOR.//2.5e-100:218:80//RATTUS NORVEGICUS (RA  
T).//P25304

F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D).//9.5e-12:29:82//HOMO SAPIENS  
(HUMAN).//Q13268

F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN.//2.4e-15:207:36//BOS TAURUS  
(BOVINE).//P04258

F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0:34:50//HOM  
O SAPIENS (HUMAN).//P39193

F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-05:49:46//NY  
CTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12.//0.97:60:33//BA  
CTERIOPHAGE PRD1.//P17637

F-HEMBA1002583

F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-15:54:55//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002592//HISTIDINE-RICH PROTEIN.//0.99:39:28//PLASMODIUM FALCIPAR

UM (ISOLATE FCM17 / SENEGAL).//P14586  
 F-HEMBA1002609//SSM4 PROTEIN.//1.9e-12:135:29//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P40318  
 F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F  
 COMPLEX SUBUNIT 6).//1.0:20:55//ZEA MAYS (MAIZE).//P19445  
 F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP  
 ROTEIN).//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-HEMBA1002628  
 F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES  
 VIRUS. (STRAIN KAPLAN) (PRV).//P33479  
 F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-16:57:68/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1002651  
 F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS ELEGAN  
 S.//P17656  
 F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//H  
 OMO SAPIENS (HUMAN).//P08547  
 F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN)  
 .//P49152  
 F-HEMBA1002678  
 F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:27//P  
 LASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816  
 F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-0  
 7:198:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804  
 F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAG  
 EN) (LC COLLAGEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388  
 F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR V  
 IRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBA1002712//11.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE P

F1.//P25133

F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS SUBTILIS  
 .//P37807

F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-18:56:75/  
 /HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS  
 JANNASCHII.//Q57764

F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//  
 SUS SCROFA (PIG).//P27917

F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT F  
 LY).//Q02910

F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BET  
 A) (GPIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400

F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-15:49:75//  
 HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.  
 //0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746

F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//0.23:88:27//ORYCTO  
 LAGUS CUNICULUS (RABBIT).//P02779

F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43  
 //MUS MUSCULUS (MOUSE).//P06798

F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REG  
 ION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880

F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS M  
 USCULUS (MOUSE).//Q60879

F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0  
 044:66:37//GLYCINE MAX (SOYBEAN).//Q10370

F-HEMBA1002801

F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.

0033:116:31//CAENORHABDITIS ELEGANS.//Q09202  
 F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.//  
 1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014308  
 F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE  
 ).//P37889  
 F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:34//BACT  
 ERIOPHAGE T4.//P16012  
 F-HEMBA1002833  
 F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//  
 METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493  
 F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I  
 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E).//0.84:37:43//SYNECHOCYSTIS SP. (S  
 TRAIN PCC 6803).//P12975  
 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.74:58:34//MUS MUSCULUS  
 (MOUSE).//Q06666  
 F-HEMBA1002886  
 F-HEMBA1002896//HOMEODOMAIN PROTEIN HOX-B3 (HOX-2G) (HOX-2.7).//4.7e-05:84:  
 35//HOMO SAPIENS (HUMAN).//P14651  
 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.21:  
 42:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1).//P0  
 5908  
 F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.85:75:22//ARABIDOPSIS  
 THALIANA (MOUSE-EAR CRESS).//Q42377  
 F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-31:92:72//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT).//7.7e  
 -06:187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18730  
 F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40.//0.00031:150:24//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./  
/5.2e-25:225:33//HOMO SAPIENS (HUMAN).//P16157

F-HEMBA1002944

F-HEMBA1002951//TRICHOHYALIN.//0.0011:220:24//HOMO SAPIENS (HUMAN).//Q07  
283

F-HEMBA1002954//PROBABLE E8 PROTEIN.//0.98:49:32//BOVINE PAPILLOMAVIRUS  
TYPE 4.//P08352

F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)  
./0.93:41:34//DROSOPHILA SEHELLIA (FRUIT FLY).//O18417

F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.00010:35:62/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002971//INSULIN.//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH  
) (PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH).//P09536

F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1  
.4.17) (DPDE4).//3.0e-29:63:100//RATTUS NORVEGICUS (RAT).//P14646

F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC R  
EGION.//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5325  
3

F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40.//0.026:175:23//SACCHAROMYCES C  
EREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-36:102:70  
//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.029:75:29//MY  
COBACTERIUM TUBERCULOSIS.//P71779

F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.3e-23:144:46  
//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC RE  
GION.//0.99:55:30//BACILLUS SUBTILIS.//P54457

F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4.//0.17:42:40//HOMO SA

PIENS (HUMAN).//P47928

F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
./0.69:28:46//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR  
(EC 3.4.24.64) (BETA-MPP) (P-52).//7.9e-124:253:96//HOMO SAPIENS (HUMAN)  
).//075439

F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.  
25:263:22//TRYPANOSOMA BRUCEI BRUCEI.//P04540

F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R  
EGION.//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321  
4

F-HEMBA1003071//CUTICLE COLLAGEN 40.//6.0e-07:126:38//CAENORHABDITIS ELE  
GANS.//P34804

F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROT  
EIN).//2.4e-12:139:34//HOMO SAPIENS (HUMAN).//Q06828

F-HEMBA1003078//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.2e-05:60:40//MUS MUSCULUS (  
MOUSE).//P11369

F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q027  
22

F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75/  
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003086

F-HEMBA1003096//PROTAMINE IA (IRIDINE IA).//0.36:20:40//SALMO IRIDEUS (R  
AINBOW TROUT).//P02328

F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-09:43:72//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHAB  
DITIS ELEGANS.//Q09456

F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MELLIFERA (HONEYBEE).//P34859

F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:37//HOMO SAPIENS (HUMAN).//P25067

F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-HEMBA1003142

F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECURSOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189

F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-13:54:66//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//035020

F-HEMBA1003197

F-HEMBA1003199//HOMEODOMAIN PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:38//HOMO SAPIENS (HUMAN).//Q00056

F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILESII (FLAT-SKULLED MARSUPIAL MOUSE).//018747

F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.2e-22:42:80//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.6e-18:74:71//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-18:56:78//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION

ION.//0.0018:159:27//BACILLUS SUBTILIS.//P46327  
 F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPS).//1.0:85:28//TRITICUM AESTIVUM (WHEAT).//P24846  
 F-HEMBA1003235//TROPOMYOSIN.//8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088  
 F-HEMBA1003250  
 F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSIFORMIS.//P21260  
 F-HEMBA1003273  
 F-HEMBA1003276  
 F-HEMBA1003278  
 F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALLUS GALLUS (CHICKEN).//P17277  
 F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.96:37:35//SULFOLOBUS ACIDOCALDARIUS.//P39472  
 F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROFA (PIG).//Q28948  
 F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49:28//BOS TAURUS (BOVINE).//P15781  
 F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:30//PROTOTHENIA WICKERHAMII.//P46750  
 F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN.//0.69:54:37//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306  
 F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06:143:22//HOMO SAPIENS (HUMAN).//Q02779  
 F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-30:53:77//HOMO SAPIENS (HUMAN).//P39194



F-HEMBA1003327

F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667

F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.5e-09:56:66//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-18:99:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003373

F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.7e-16:60:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-10:50:68//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003384

F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927

F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04521

F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481

F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33301

F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-09:239:33//NEPHILA CLAVIPES (ORB SPIDER).//P19837

F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497

F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127

F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451

F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-18:56:78//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e-28:136:47//HOMO SAPIENS (HUMAN).//P00736

F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105:217:85//RATTUS NORVEGICUS (RAT).//P50480

F-HEMBA1003548

F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558

F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGION (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706

F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.8e-32:71:100//BOS TAURUS (BOVINE).//P16874

F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//4.1e-19:126:31//HOMO SAPIENS (HUMAN).//P14373

F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//3.9e-83:143:74//HOMO SAPIENS (HUMAN).//Q13330

F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D).//1.0:64:25//STAPHYLOCOCCUS AUREUS.//P03860

F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1).//1.0:41:29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01448

F-HEMBA1003581//TALIN.//3.7e-36:52:98//MUS MUSCULUS (MOUSE).//P26039

F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P19682

F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

F-HEMBA1003597

F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//4.9e-10:85:41//ORYZOLAGUS CUNICULUS (RABBIT).//P06333

F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43).//0.086:10:70//BACTERIOPHAGE PHI-LF.//Q07482

F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I.//4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10169

F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A).//0.096:40:37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P01387

F-HEMBA1003622

F-HEMBA1003630

F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:47:74//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.87:25:64//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.8e-10:157:26//CAENORHABDITIS ELEGANS.//Q17963

F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED ) (52-KD BRACKETING PROTEIN) (B52 PROTEIN).//4.9e-05:207:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26686

F-HEMBA1003656

F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B.//0.57:17:52//HOMO SAPIENS (HUMAN).//P02814

F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.0e-16:43:72//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003679

F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3. 4.11.-).//3.9e-08:137:27//CAENORHABDITIS ELEGANS.//P34629

F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//2.1e-20:127:40//MUS MUSCULUS (MOUSE).//Q60821

F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//3.0e-85:201:78//HOMO SAPIENS (HUMAN).//P56524

F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1.//0.13:69:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986

F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN).//0.021:153:26//HOMO SAPIENS (HUMAN).//P06731

F-HEMBA1003714//ABAECIN.//0.99:34:32//BOMBUS PASCUORUM.//P81463

F-HEMBA1003715

F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4e-34:155:56//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-27:181:41//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.0037:103:33//HOMO SAPIENS (HUMAN).//P23246

F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-54:210:58//H

OMO SAPIENS (HUMAN).//P08547  
F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.066:72:33//DROSO  
PHILA MELANOGASTER (FRUIT FLY).//Q01643  
F-HEMBA1003758  
F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT  
ERACTING PROTEIN).//1.5e-51:220:52//MUS MUSCULUS (MOUSE).//Q61221  
F-HEMBA1003773  
F-HEMBA1003783  
F-HEMBA1003784  
F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C).//0.95:27:37//ACANTHOPHI  
S ANTARCTICUS (COMMON DEATH ADDER).//P01434  
F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].  
//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338  
F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
.//0.019:30:50//HOMO SAPIENS (HUMAN).//P30808  
F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III.  
//1.8e-20:109:47//CAENORHABDITIS ELEGANS.//P42083  
F-HEMBA1003807  
F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.1e-09:2  
3:78//OWENIA FUSIFORMIS.//P21260  
F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//2.0e-31:134:52//SACCHAROM  
YCES CEREVISIAE (BAKER'S YEAST).//P40484  
F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.9e-22:39:76/  
/HOMO SAPIENS (HUMAN).//P39192  
F-HEMBA1003856  
F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REG  
ION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151  
F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPEN  
HAGEN).//P21062

F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161

F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIS CATUS (CAT).//P48896

F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215

F-HEMBA1003902

F-HEMBA1003908

F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-10:60:63//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.1e-29:68:64//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637

F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (071).//0.95:26:34//ESCHERICHIA COLI.//P46878

F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003959

F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOMO SAPIENS (HUMAN).//Q14999

F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.9

8:19:57//HOMO SAPIENS (HUMAN).//P22531  
 F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE)  
 (LYSRS) (FRAGMENT).//1.0:40:32//MYCOBACTERIUM LEPRAE.//P46861  
 F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66.//0.27:65:33//HUMAN CYTOMEGALO  
 VIRUS (STRAIN AD169).//P16822  
 F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB.//5.2e-05:64:40//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-HEMBA1004000//PROTEIN Q300.//0.00042:17:82//MUS MUSCULUS (MOUSE).//Q02  
 722  
 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CG  
 RP-I).//0.47:106:32//HOMO SAPIENS (HUMAN).//P06881  
 F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIP  
 ID-BINDING PROTEIN).//0.96:36:33//PARAMECIUM TETRAURELIA.//P16001  
 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III./  
 /0.00018:90:34//CAENORHABDITIS ELEGANS.//P41997  
 F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-34:75:80/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1004038  
 F-HEMBA1004042  
 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A.//1.0:20:55//ASPARAGUS OFFICI  
 NALIS (GARDEN ASPARAGUS).//P31753  
 F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3e-06:158:35//M  
 US MUSCULUS (MOUSE).//P05143  
 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN).//0.098:106:32//D  
 ICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54658  
 F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259.//0.87:133:23//HAEMOPHIL  
 US INFLUENZAE.//P43974  
 F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.3e-25:39:64  
 //HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.9e-08:35:68//  
HOMO SAPIENS (HUMAN).//P39188  
F-HEMBA1004086  
F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT).//0.71:95:  
35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379  
F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-26:84:64//  
HOMO SAPIENS (HUMAN).//P39188  
F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIE  
NS (HUMAN).//Q14141  
F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736.//1.0:44:34//HAEMOPHILUS INF  
LUENZAE.//P44300  
F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCO  
BACTERIUM TUBERCULOSIS.//Q10826  
F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:4  
1//MEDICAGO SATIVA (ALFALFA).//P11728  
F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.  
3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039  
F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO  
SAPIENS (HUMAN).//P02811  
F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MO  
USE).//P02798  
F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.0e-13:57:71/  
/HOMO SAPIENS (HUMAN).//P39195  
F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+  
)- TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE./  
/P43437  
F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-1  
4:115:31//CAENORHABDITIS ELEGANS.//P34529  
F-HEMBA1004200



F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P11620  
F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-09:48:64//HOMO SAPIENS (HUMAN).//P39193  
F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
F-HEMBA1004225//METALLOTHIONEIN-II.//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114  
F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (K1AA0015).//5.9e-06:109:33//HOMO SAPIENS (HUMAN).//P49593  
F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN.//0.98:39:38//ESCHERICHIA COLI.//P05056  
F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT).//0.66:36:38//MUS MUSCULUS (MOUSE).//Q04891  
F-HEMBA1004246  
F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//1.0e-43:98:84//RATTUS NORVEGICUS (RAT).//Q08755  
F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.014:160:28//NEPHILA CLAVIPES (ORB SPIDER).//P46804  
F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-52:56:83//HOMO SAPIENS (HUMAN).//P39189  
F-HEMBA1004272  
F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III.//0.00084:33:54//CAENORHABDITIS ELEGANS.//P34485  
F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//9.3e-06:125:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40034  
F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A).//3.7e-30:239:32//HOMO SAPIENS (HUMAN).//Q10567

F-HEMBA1004286//CUTICLE COLLAGEN 34.//0.0027:71:38//CAENORHABDITIS ELEGANS.//P34687

F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN).//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43606

F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.075:58:39//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORGANIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P27946

F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//4.3e-43:133:44//MUS MUSCULUS (MOUSE).//Q61967

F-HEMBA1004323

F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIENS (HUMAN).//P35326

F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOMO SAPIENS (HUMAN).//Q05925

F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-24:41:80//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//MUS MUSCULUS (MOUSE).//P05143

F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.2e-29:57:80//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22516

F-HEMBA1004356

F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HOMO SAPIENS (HUMAN).//P39195

MO SAPIENS (HUMAN).//P08547  
F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME  
I.//1.0:125:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263  
F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC RE  
GION.//0.76:170:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893  
F-HEMBA1004394  
F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HO  
MO SAPIENS (HUMAN).//P08547  
F-HEMBA1004405  
F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPI  
ASE) (ROTAMASE) (CYCLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGAN  
S.//P52017  
F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//0.0019:47:59/  
/HOMO SAPIENS (HUMAN).//P39191  
F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-20:47:68/  
/HOMO SAPIENS (HUMAN).//P39192  
F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.2e-64:134:69  
//HOMO SAPIENS (HUMAN).//P39193  
F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVU  
M (GARDEN PEA).//P20830  
F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT  
ERACTING PROTEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221  
F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDID  
A GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P05040  
F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGA  
NS.//P52275  
F-HEMBA1004502  
F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3e-11:119:35//MUS MUSC  
ULUS (MOUSE).//P11260

F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.  
00072:90:37//HOMO SAPIENS (HUMAN).//Q15428

F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC RE  
GION.//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589

F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE F  
ILAMIN) (FILAMIN 1).//1.3e-80:226:66//HOMO SAPIENS (HUMAN).//P21333

F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS  
JANNASCHII.//Q58174

F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTI  
C COD).//P51902

F-HEMBA1004554

F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//  
HOMO SAPIENS (HUMAN).//Q92556

F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PL  
ASMODIUM BERGHEI.//P06915

F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-08:35:80/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.6e-08:64:54/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNR  
NP CORE PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT)./  
/P17132

F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:  
37:45//MUS MUSCULUS (MOUSE).//Q64739

F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-11:73:54//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004617

F-HEMBA1004629

F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGI

ON.//1.0:36:38//BACILLUS SUBTILIS.//P42303  
 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT  
 -HARVESTING 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NA  
 EGELI.//P20453  
 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III./  
 /1.7e-32:159:42//CAENORHABDITIS ELEGANS.//P34535  
 F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:5  
 0:46//OWENIA FUSIFORMIS.//P21260  
 F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (E  
 ASTERN JAMESON' S MAMBA).//P25682  
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
 NG FACTOR SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170  
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//  
 HOMO SAPIENS (HUMAN).//P02452  
 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS  
 JANNASCHII.//Q57879  
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HE  
 AVY CHAIN, TYPE B) (NMMHC-B).//0.00035:217:23//HOMO SAPIENS (HUMAN).//P3  
 5580  
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H)  
 .//0.058:118:30//STREPTOCOCCUS PYOGENES.//P50470  
 F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.8e-09:43:72//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.8e-18:50:84/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//0  
 .0027:148:30//HOMO SAPIENS (HUMAN).//O00321  
 F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS ELEGAN  
 S.//P17656

F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-07:50:62//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBI  
QUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9e-39:143  
:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.1e-60:210:61//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1004748

F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.8e-20:88:63//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
0043:126:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-28:47:78/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REG  
ION.//0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981

F-HEMBA1004758

F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:5  
8:43//OWENIA FUSIFORMIS.//P21260

F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:298:53//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1004770

F-HEMBA1004771

F-HEMBA1004776//GRANULIN 1.//0.78:28:42//CYPRINUS CARPIO (COMMON CARP)./  
/P81013

F-HEMBA1004778

F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//6.9e-20:74:63//HOMO SAPIE

NS (HUMAN).//P50851  
 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:58:86//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182).//0.72:75:33//CYANOPHORA PARADOXA.//P48324  
 F-HEMBA1004807  
 F-HEMBA1004816  
 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT).//1.0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).//P26226  
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e-76:171:91//CANIS FAMILIARIS (DOG).//Q00004  
 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.0e-05:64:43//BOS TAURUS (BOVINE).//P25508  
 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR.//0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329  
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612  
 F-HEMBA1004865  
 F-HEMBA1004880  
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.66:23:47//HOMO SAPIENS (HUMAN).//P22532  
 F-HEMBA1004900  
 F-HEMBA1004909  
 F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:37:32//SPINACIA OLERACEA (SPINACH).//P09597  
 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-24:44:68//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38/

/STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997  
 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:41//HOMO SAPIENS (HUMAN).//P50552  
 F-HEMBA1004934  
 F-HEMBA1004944  
 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.58:78:30//PARAMECIUM TETRAURELIA.//P15579  
 F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM TETRAURELIA.//P15605  
 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN (ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA COLI.//P21324  
 F-HEMBA1004972  
 F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS (HUMAN).//P22531  
 F-HEMBA1004977  
 F-HEMBA1004978  
 F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811  
 F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA APHIDICOLA.//Q59176  
 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080  
 F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYSTER).//P23038  
 F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P1423



F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS IN  
FLUENZAE.//P44129

F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).  
//0.76:72:31//GALLUS GALLUS (CHICKEN).//P32250

F-HEMBA1005035//HOMEBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN  
) .//P50219

F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.  
47:49:32//HOMO SAPIENS (HUMAN).//P22532

F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MU  
S MUSCULUS (MOUSE).//P35290

F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//B  
OS TAURUS (BOVINE).//P25508

F-HEMBA1005062

F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CER  
EVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.6e-20:75:64  
//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34/  
/BOS TAURUS (BOVINE).//P25508

F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (  
HRP48.1).//4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809

F-HEMBA1005113

F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-24:99:60/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REG  
ION.//0.11:22:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-16:59:71//

HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEIN  
 ASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN]../1.0:77:27//BARLEY YELLOW MO  
 SAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV).//Q01207  
 F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .40:53:33//APIS MELLIFERA (HONEYBEE).//P34859  
 F-HEMBA1005185//MYOSIN IB HEAVY CHAIN../0.011:58:48//DICTYOSTELIUM DISCO  
 IDEUM (SLIME MOLD).//P34092  
 F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I../  
 3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09817  
 F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.8e  
 -124:257:95//CANIS FAMILIARIS (DOG).//Q00004  
 F-HEMBA1005206//CUTICLE COLLAGEN 1../0.010:118:33//CAENORHABDITIS ELEGAN  
 S../P08124  
 F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40//HOMO  
 SAPIENS (HUMAN).//P23246  
 F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN../0.31:75:28//BACTERIOPHA  
 GE T3../P07715  
 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN../0.99:48:29//VACCINIA VIRUS  
 (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P20544  
 F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-28:138:55  
 //HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
 14:39:41//HOMO SAPIENS (HUMAN).//P22531  
 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:15:46/  
 /DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362  
 F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.0  
 88:33:42//ZEA MAYS (MAIZE).//P43401  
 F-HEMBA1005274

F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.96:42:45//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168

F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:34//HOMO SAPIENS (HUMAN).//Q02817

F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-33:103:74//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY).//Q04536

F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III.//0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009

F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:51//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT).//0.57:44:38//GALLUS GALLUS (CHICKEN).//Q98913

F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1005338//CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//1.8e-55:199:59//GALLUS GALLUS (CHICKEN).//P05099

F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:36//PORPHYRA PURPUREA.//P51305

F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.1e-68:255:48//HOMO SAPIENS (HUMAN).//P51522

F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER).//P80403

F-HEMBA1005372

F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:92:75//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII).//0.99:39:33//BOS TAURUS (BOVINE).//P19034

F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3' REGION (ORF4).//0.82:164:31//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P42377

F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION .//0.98:44:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV ).//P41703

F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.066:64:29 //MUS MUSCULUS (MOUSE).//P07978

F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33.//0.77:32:25//BACILLUS SUBTILI S.//Q06798

F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//0.0065:38:52//MUS MUSCULUS (M OUSE).//P11369

F-HEMBA1005411//TOXIN S4C8.//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE ( EASTERN JAMESON' S MAMBA).//P25683

F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-D EPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//4.3e-09:29:96//HOMO SAPIENS (HUMAN).//P42773

F-HEMBA1005426//TOXIN C10S2C2.//0.99:49:34//DENDROASPIS ANGUSTICEPS (EAS TERN GREEN MAMBA).//P25684

F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:78:60// HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:57:31/ /DASYPUS NOVENMCINCTUS (NINE-BANDED ARMADILLO).//021329

F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRA GMENTS).//0.68:41:31//ARTEMIA SALINA (BRINE SHRIMP).//P19040

F-HEMBA1005469

F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-39:142:70//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.8e-10:44:68//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRP70).//9.2e-14:179:33//HOMO SAPIENS (HUMAN).//P08621

F-HEMBA1005497

F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37.//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD FLUKE).//044125

F-HEMBA1005506

F-HEMBA1005508

F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.5e-30:92:73//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//2.0e-39:95:61//DROSOPHILA MELANOGASTER (FRUIT FLY).//002193

F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.1e-06:56:44//MUS MUSCULUS (MOUSE).//P05142

F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//5.8e-05:192:33//BOS TAURUS (BOVINE).//P02453

F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.0e-18:87:57//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//5.1e-22:77:54//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.2e-81:157:98//MUS MUSCULUS (MOUSE).//Q60809

F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A).//0.98:19:47//AMBROSIA PSILOSTACHYA (WESTERN RAGWEED).//P43174

F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1.//1.4e-72:137:97//RATTUS NORVEGICUS (RAT).//P54842

F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-29:47:78/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC RE  
GION.//1.6e-20:202:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04272

F-HEMBA1005568

F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).//1.  
0:80:31//CAENORHABDITIS ELEGANS.//P24885

F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:75//HO  
MO SAPIENS (HUMAN).//P51805

F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A.//0.98:57:36//O  
VIS ARIES (SHEEP).//P02438

F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//P24014

F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYP  
EPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGIC  
US (RAT).//P28023

F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83  
:119:23//KLEBSIELLA PNEUMONIAE.//Q48453

F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:108:53/  
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.  
23:24:54//HOMO SAPIENS (HUMAN).//P22532

F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.7e-39:257:39//D  
ICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036

F-HEMBA1005606

F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-20:27:96/  
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIO  
PHAGE 186.//P08711

F-HEMBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CER  
EVISIAE (BAKER'S YEAST).//P40958

F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.18:100  
:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1005631

F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS  
(STRAIN WR).//P04309

F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-14:93:58//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAP  
IENS (HUMAN).//Q14142

F-HEMBA1005670

F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HO  
MO SAPIENS (HUMAN).//P08547

F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIE  
NS (HUMAN).//P35326

F-HEMBA1005685

F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINAS  
E LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).  
//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768

F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005717

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7).//0.22:55:41//OVIS ARIES (  
SHEEP).//P50415

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY  
SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P  
25296

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HO

MO SAPIENS (HUMAN).//P08547  
 F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-19:60:63/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOM  
 ESTIC PIGEON).//P15786  
 F-HEMBA1005813  
 F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCI  
 UM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//G  
 ALLUS GALLUS (CHICKEN).//P00789  
 F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q027  
 22  
 F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:96:73/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:46//N  
 YCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MU  
 S MUSCULUS (MOUSE).//P05143  
 F-HEMBA1005853//HYPOTHETICAL PROTEIN MJ0647.//0.39:28:39//METHANOCOCCUS  
 JANNASCHII.//Q58063  
 F-HEMBA1005884  
 F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERI  
 UM THERMOAUTOTROPHICUM.//O26240  
 F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-29:81:71/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III.//  
 0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958  
 F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-27:86:70//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-38:99:81/



/HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e-17:76:51//HOMO SAPIENS (HUMAN).//P51522  
 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.024:54:40//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBA1005962  
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620  
 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAPIENS (HUMAN).//Q15034  
 F-HEMBA1005999  
 F-HEMBA1006002  
 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267  
 F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1.//0.00016:84:39//HOMO SAPIENS (HUMAN).//P04281  
 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154  
 F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.2e-64:150:74//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1006042  
 F-HEMBA1006067//METALLOTHIONEIN A (MT-A).//0.86:34:41//THERMARCUS CERBERUS.//P52721  
 F-HEMBA1006081  
 F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:35:54//SUS SCROFA (PIG).//P31636

F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.1e-09:58:60//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1).//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902

F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTHERMOPHILUS.//P23375

F-HEMBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794

F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-13:41:73//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-39:101:77//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT).//P05432

F-HEMBA1006158

F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//0.017:20:95//HOMO SAPIENS (HUMAN).//P54829

F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.37:31:61//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23).//0.85:61:29//MUS MUSCULUS (MOUSE).//P09026

F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33.//1.0:26:38//AQUIFEX AEOLICUS.//067756

F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0041:64:37//DROS

OPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3.//1.0:22:40//

DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE).//P01057

F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATIO  
N INHIBITOR).//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER).//P

22826

F-HEMBA1006259

F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-05:32:65/  
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2).//4.8e-11  
2:248:78//HOMO SAPIENS (HUMAN).//P10264

F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
DENYLYLTRANSFERASE) (FRAGMENT).//2.5e-71:164:75//HOMO SAPIENS (HUMAN).//  
P51003

F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32.//0.81:27:44//THERMUS AQUATICU  
S (SUBSP. THERMOPHILUS).//P80339

F-HEMBA1006284//CUTICLE COLLAGEN 2.//0.36:42:40//CAENORHABDITIS ELEGANS.  
//P17656

F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGI  
ON.//2.4e-37:143:31//ESCHERICHIA COLI.//P76518

F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.//0.20:134  
:29//RATTUS NORVEGICUS (RAT).//Q63345

F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG  
ION.//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA)  
(NECTADRIN).//0.71:46:39//RATTUS NORVEGICUS (RAT).//Q07490

F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID  
PHOSPHOPROTEIN).//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5  
/73).//P32531

F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//0.98:26:  
46//ARCHAEOGLOBUS FULGIDUS.//028646

F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2).//8.8e-08:91:36//MUS  
MUSCULUS (MOUSE).//P26040

F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//9.1e-48  
:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//002193

F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1.//0.015:59:33//CASUARINA  
GLAUCA (SWAMP OAK).//Q39511

F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261  
:66//HOMO SAPIENS (HUMAN).//P28160

F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//0.97:60:3  
5//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10348

F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20).//0.00023:110:35//MEDI  
CAGO TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1006380

F-HEMBA1006381//METALLOTHIONEIN-II.//1.0:26:38//CANDIDA GLABRATA (YEAST)  
(TORULOPSIS GLABRATA).//P15114

F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.3e-26:123:52//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1006416

F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-24:102:50  
//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:101:57/  
/HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVI  
RUS (STRAIN MEBUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053

F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-36:78:74/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLAR

DIA THETA (CRYPTOMONAS PHI).//078421  
 F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS  
 (MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280  
 F-HEMBA1006446  
 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.1e-18:68:67/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBA1006467  
 F-HEMBA1006471  
 F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV  
 ).//Q01552  
 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.1e-38:77:74/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGI  
 ON (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465  
 F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BA  
 KER'S YEAST).//P32907  
 F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3)  
 (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HU  
 MAN).//015239  
 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZ  
 OBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//P42711  
 F-HEMBA1006497  
 F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.15:26:73//HOM  
 O SAPIENS (HUMAN).//P39188  
 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGAS  
 TER (FRUIT FLY).//P48608  
 F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100

) (3-KETOACYL- ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERI  
CHIA COLI.//P25716

F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA  
GMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)  
.//P15583

F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e  
-05:53:39//MUS MUSCULUS (MOUSE).//008863

F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97  
) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q  
62696

F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS T  
YPE 51.//P26553

F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES C  
EREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//  
1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163

F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLO  
G EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG)  
.//P23437

F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BO  
S TAURUS (BOVINE).//P02465

F-HEMBA1006579

F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS M  
USCULUS (MOUSE).//P05142

F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.6e-34:93:77/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.9e-26:75:74/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES C

EREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.6e-20:73:63//

HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506

F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5333

1

F-HEMBA1006635

F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN

1) (PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341

F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817

F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014

F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS (MOUSE).//P14148

F-HEMBA1006653

F-HEMBA1006659

F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//000268

F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:51//OWENIA FUSIFORMIS.//P21260

F-HEMBA1006682

F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006696

F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
IN PMC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIA  
E (BAKER'S YEAST).//P53196

F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPI  
ENS (HUMAN).//P28702

F-HEMBA1006717

F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR  
OID) (FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485

F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78  
//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (C  
ADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (H  
UMAN).//P33151

F-HEMBA1006767

F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHM  
ANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940

F-HEMBA1006780

F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS  
MUSCULUS (MOUSE).//P05143

F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//N  
YCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:3  
8:42//MUS MUSCULUS (MOUSE).//P70315

F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.  
//4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568

F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//H



OMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q  
 01229  
 F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III./  
 /1.0:46:36//CAENORHABDITIS ELEGANS.//P34327  
 F-HEMBA1006849  
 F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II).//1.0:41:31//BO  
 S TAURUS (BOVINE).//P01001  
 F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS  
 CUNICULUS (RABBIT).//P16258  
 F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//  
 4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057  
 F-HEMBA1006900  
 F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACT  
 ING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST  
 ).//P52488  
 F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLE  
 UCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473  
 F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN  
 ).//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258  
 F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS  
 JANNASCHII.//Q57945  
 F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSO  
 R (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C  
 ) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS (HUMAN).//P02810  
 F-HEMBA1006938  
 F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA  
 TABACUM (COMMON TOBACCO).//P29449  
 F-HEMBA1006949

F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//P25508

F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206

F-HEMBA1006993

F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A).//0.00096:60:33//HOMO SAPIENS (HUMAN).//P14770

F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION.//1.0:25:56//ESCHERICHIA COLI.//P39166

F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828

F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007051

F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402

F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29//RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063

F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.58:49:38//BOMBYX MORI (SILK MOTH).//P25331

F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696

F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM D  
ISCOIDEUM (SLIME MOLD).//P54681

F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOC  
CUS JANNASCHII.//Q57626

F-HEMBA1007112

F-HEMBA1007113

F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP)  
.//5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441

F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL L  
EECH).//P80302

F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REG  
ION.//0.92:23:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

F-HEMBA1007149//BACTERIOCIN MICROGIN B17 PRECURSOR (MCB17).//0.0078:17:7  
0//ESCHERICHIA COLI.//P05834

F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS (MOUS  
E).//Q62477

F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REG  
ION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.8e-06:38:65/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFOR  
M PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON  
TOBACCO).//Q43793

F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845

F-HEMBA1007206

F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.//  
2.4e-05:92:30//CAENORHABDITIS ELEGANS.//Q09275

F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE).//P00493

F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238

F-HEMBA1007256

F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN).//Q13939

F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421

F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.6e-24:98:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007281

F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162

F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156

F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:33//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1007319

F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672

F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:33//ESCHERICHIA COLI.//P11866

F-HEMBA1007327

F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.1e-12:37:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE PAPIL

LOMAVIRUS TYPE 1.//Q02268  
 F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400  
 F-HEMBB1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA).//P29179  
 F-HEMBB1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.7e-35:73:84//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBB1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AGROBACTERIUM TUMEFACIENS.//P08061  
 F-HEMBB1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494  
 F-HEMBB1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-HEMBB1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576  
 F-HEMBB1000037//HYPOTHETICAL 59.9 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492  
 F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219  
 F-HEMBB1000044  
 F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS.//P54942  
 F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-14:34:79//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.9e-31:45:73//HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DENDROASP  
IS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-21:82:59/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN;  
BETA-GRANIN; WE-14] .//0.87:172:28//RATTUS NORVEGICUS (RAT).//P10354

F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGI  
ON (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879

F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//7.7e-08:31:87/  
/HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-13:57:64//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169

F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC RE  
GION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327

F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34  
:64//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.0e-26:81:69  
//HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-29:91:71//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQ  
UUS CABALLUS (HORSE).//P80930

F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:52//  
PORPHYRA PURPUREA.//P51329

F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:39:76/  
/HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//2.9  
e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38/  
/MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949

F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//  
6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217

F-HEMBB1000240

F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-05:44:61//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000250

F-HEMBB1000258

F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEG  
ANS.//P12114

F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:22//SAC  
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730

F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).  
//0.75:30:43//BOS TAURUS (BOVINE).//P00429

F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL P  
ROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SCROFA (PIG)./  
/P35323

F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30//MUS M  
USCULUS (MOUSE).//Q09098

F-HEMBB1000307

F-HEMBB1000312

F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO SAPIEN  
S (HUMAN).//P07996

F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN N  
S3) (NONSTRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORONAVIRUS (STRA  
IN OC43).//Q04854

F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT).//0.82:33:45//MUS MUSCULUS (MOUSE).//P10754

F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:44:40//ORYCTOLAGUS CUNICULUS (RABBIT).//P80456

F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-14:54:55//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPHAGE L5.//Q05289

F-HEMBB1000343

F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:83:56//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.7e-34:56:78//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1000376

F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:79:35//BOS TAURUS (BOVINE).//P25508

F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50531

F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583

F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//CYANOPHORA PARADOXA.//P48129

F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.



023:97:35//HOMO SAPIENS (HUMAN).//Q15427  
 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.8e-20:111:54  
 //HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGI  
 ON.//0.93:24:50//BACTERIOPHAGE T4.//P07076  
 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-23:85:70//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.88:27:51//HO  
 MO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000455  
 F-HEMBB1000472  
 F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P11905  
 F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II).//  
 0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//P01427  
 F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.3e-16:50:80/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000491  
 F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRU  
 S (STRAIN BEAUDETTE) (IBV).//P30237  
 F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//H  
 OMO SAPIENS (HUMAN).//P08547  
 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.02  
 1:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546  
 F-HEMBB1000523  
 F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-1  
 4:43:83//GALLUS GALLUS (CHICKEN).//P32018  
 F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.  
 19:97:30//TRYPANOSOMA BRUCEI BRUCEI.//P04540  
 F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS

LAEVIS (AFRICAN CLAWED FROG).//P40744  
 F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
 FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS  
 (HUMAN).//000268  
 F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:52:34//  
 METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493  
 F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.3e-10:52:73  
 //HOMO SAPIENS (HUMAN).//P39191  
 F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-26:76:76/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3)  
 (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HU  
 MAN).//000483  
 F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.9e-25:61:75/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//  
 PETROMYZON MARINUS (SEA LAMPREY).//Q35537  
 F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPI  
 ENS (HUMAN).//P35326  
 F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32/  
 /GALLUS GALLUS (CHICKEN).//P12105  
 F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:41//N  
 YCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III./  
 /0.0022:98:28//CAENORHABDITIS ELEGANS.//P34284  
 F-HEMBB1000630  
 F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR)  
 (SUBTYPE C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825  
 F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:17

3:28//MUS MUSCULUS (MOUSE).//P27671  
 F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.6e-41:94:82/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P074  
 76  
 F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.3e-30:77:76/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-37:58:81/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-37:61:77/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA BURGD  
 O RFERI (LYME DISEASE SPIROCHETE).//P70845  
 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-  
 IB) (ST-H).//0.012:37:37//ESCHERICHIA COLI.//P07965  
 F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.1e-21:66:72/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:49/  
 /RATTUS NORVEGICUS (RAT).//P54256  
 F-HEMBB1000705  
 F-HEMBB1000706  
 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW M  
 OSAIC VIRUS (CYMV).//P16485  
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS NOR  
 VEGICUS (RAT).//P70550  
 F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:85:70/  
 /HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS  
(SUBSP. THERMOPHILUS).//P35871

F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-29:42:85/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045

F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (G  
UINEA PIG).//P22075

F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUS  
CULUS (MOUSE).//P17095

F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (ME  
KK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083

F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERG  
ENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./  
/P39956

F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:93:51//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000794

F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALL  
US GALLUS (CHICKEN).//P49578

F-HEMBB1000810

F-HEMBB1000821

F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISS  
US MOSAIC VIRUS (NMV).//P15099

F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73  
:39//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS  
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPH  
ILA MELANOGASTER (FRUIT FLY).//P08175

F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBB1000852  
F-HEMBB1000870  
F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725  
F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//078459  
F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251  
F-HEMBB1000888  
F-HEMBB1000890  
F-HEMBB1000893  
F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552  
F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.29:56:46//HOMO SAPIENS (HUMAN).//P39195  
F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156  
F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193  
F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614

F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326

F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:66:36//BOS TAURUS (BOVINE).//018739

F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG).//0.00042:77:41//HOMO SAPIENS (HUMAN).//P04196

F-HEMBB1000981

F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575

F-HEMBB1000991

F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.58:34:35//ESCHERICHIA COLI.//P33669

F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B.//P26550

F-HEMBB1001008

F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN).//P17097

F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN).//1.0:58:39//RATTUS NORVEGICUS (RAT).//P97545

F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.4e-07:36:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1001024

F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203

F-HEMBB1001047

F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION).

//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636  
 F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//OR  
 GYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341  
 F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-33:95:76/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1  
 .0:38:36//CAENORHABDITIS ELEGANS.//P34591  
 F-HEMBB1001063  
 F-HEMBB1001068  
 F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROID  
 ES NOXIUS (MEXICAN SCORPION).//P08815  
 F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1  
 .1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECU  
 RSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067  
 F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126  
 :287:85//RATTUS NORVEGICUS (RAT).//P38378  
 F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//BACTERI  
 OPHAGE L2.//P42537  
 F-HEMBB1001117  
 F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//H  
 OMO SAPIENS (HUMAN).//Q99715  
 F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//  
 1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296  
 F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-09:53:62/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMS  
 TER).//P11414

F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.1e-05:46:56/  
/HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//  
2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:34//AS  
CARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393

F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:71:59/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357

F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:27//  
HOMO SAPIENS (HUMAN).//Q15269

F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROM  
YCES CEREVISIAE (BAKER'S YEAST).//P54858

F-HEMBB1001199

F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCU  
LUS (MOUSE).//P15974

F-HEMBB1001209

F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCUL  
US (MOUSE).//P15974

F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-19:49:67/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (E  
C 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406

F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//M  
US MUSCULUS (MOUSE).//P46938

F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN  
C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE  
(FISSION YEAST).//Q09876

F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.



0:23:43//KLEBSIELLA PNEUMONIAE.//P13155  
 F-HEMBB1001253//METALLOTHIONEIN-1H (MT-1H) (METALLOTHIONEIN-0) (MT-0).//  
 0.14:16:43//HOMO SAPIENS (HUMAN).//P80294  
 F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-12:40:75/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-12:33:78/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1  
 .0:58:37//CAENORHABDITIS ELEGANS.//Q10928  
 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM V  
 INOSUM.//Q06527  
 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHER  
 ICHIA COLI.//P46719  
 F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSC  
 ULUS (MOUSE).//P11260  
 F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (  
 HUMAN).//P17081  
 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2)  
 (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626  
 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1)  
 (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157  
 F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DRO  
 SOPHILA ERECTA (FRUIT FLY).//P13730  
 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-24:53:71/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//  
 0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782  
 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCUL  
 US (MOUSE).//P15974

F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VI  
 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//  
 SCIARA COPROPHILA (FUNGUS GNAT).//Q01799  
 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.2e-20:62:62/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:34  
 //MYCOBACTERIUM TUBERCULOSIS.//Q50606  
 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-14:61:62//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001356  
 F-HEMBB1001364  
 F-HEMBB1001366//HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPAR  
 UM (ISOLATE FCM17 / SENEGAL).//P14586  
 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//8.6e-40:146:61  
 //HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001369  
 F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.9e-25:49:83/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29/  
 /MUS MUSCULUS (MOUSE).//P70444  
 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCE  
 S CEREVISIAE (BAKER'S YEAST).//P40091  
 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP  
 HA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADA  
 PTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE)  
 .//P17426

F-HEMBB1001410

F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//  
0.99:37:21//ORYZA SATIVA (RICE).//P12162

F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:40:60//  
HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTI  
DASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.  
5) (PROLYL AMINOPEPTIDASE).//1.1e-99:219:86//BOS TAURUS (BOVINE).//P0072  
7

F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-30:57:78/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURS  
OR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SU  
BUNIT) (PDPC).//2.5e-79:155:97//BOS TAURUS (BOVINE).//P35816

F-HEMBB1001449

F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161

F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAU  
DI.//P14592

F-HEMBB1001463

F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPA  
RUM (ISOLATE PALO ALTO / UGANDA).//P07765

F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLCGF16.1 (FRAGMENT).//4.2e  
-10:37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18712

F-HEMBB1001500

F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-39:59:72//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001527//HOMEBOX PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT).  
//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019

F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L  
5.//Q05241

F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//  
LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-HEMBB1001536

F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//0.0063:52:50/  
/HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.9e-23:69:63//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P  
47709

F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//H  
OMO SAPIENS (HUMAN).//P08547

F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.9e-12:51:54/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001585

F-HEMBB1001586

F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REG  
ION.//0.0031:31:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

F-HEMBB1001603

F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//0.00076:47:44//MUS MUSCULUS (  
MOUSE).//P11369

F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//1.0  
:52:32//HOMO SAPIENS (HUMAN).//P22531

F-HEMBB1001630

F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A.//1.0:27:44//LYCOP  
ERSICON ESCULENTUM (TOMATO).//Q40157

F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0042:26:73//H

OMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001641  
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1.//0.51:36:47//CANIS FAMILIARIS (DOG).//002771  
 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.0030:135:34//HOMO SAPIENS (HUMAN).//Q05925  
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39.//0.99:25:44//CAENORHABDITIS ELEGANS.//P52814  
 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38823  
 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40.//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIB) (IX).//1.0:21:47//BOS TAURUS (BOVINE).//P10175  
 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN.//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569  
 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.91:39:41//SUS SCROFA (PIG).//P35323  
 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//1.0:43:23//BRADYRHIZOBIUM JAPONICUM.//P27394  
 F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT).//1.0:71:25//LEMUR CATTAL (RING-TAILED LEMUR).//Q34878  
 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-35:97:74//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110).//0.00069:180:28//HOMO SAPIENS (HUMAN)

AN).//P55884  
 F-HEMBB1001747  
 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-43:75:70/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001753//PROTEIN Q300.//0.00091:16:81//MUS MUSCULUS (MOUSE).//Q02  
 722  
 F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9).//  
 0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91879  
 F-HEMBB1001760  
 F-HEMBB1001762//GENE 35 PROTEIN (GP35).//0.76:21:47//MYCOBACTERIOPHAGE L  
 5.//Q05245  
 F-HEMBB1001785  
 F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//0.99:41:31//PORP  
 HYRA PURPUREA.//P51270  
 F-HEMBB1001802  
 F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-39:54:77/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-19:97:57/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN. IN COX5A-ALG11 INTERGENIC R  
 EGION.//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53951  
 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT).//0.0014:4  
 0:45//SORGHUM VULGARE (SORGHUM).//Q99069  
 F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//7.1e-14:85:61  
 //HOMO SAPIENS (HUMAN).//P39191  
 F-HEMBB1001839//PROBABLE E4 PROTEIN.//0.61:49:34//HUMAN PAPILLOMAVIRUS T  
 YPE 6C.//P20969  
 F-HEMBB1001850  
 F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-30:57:68/

/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1001867

F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP  
ROTEIN).//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-11:95:45//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION  
.//1.0:34:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV)  
.//P41459

F-HEMBB1001874

F-HEMBB1001875

F-HEMBB1001880

F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2  
B.//P15902

F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REG  
ION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234

F-HEMBB1001906

F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80/  
/HOMO SAPIENS (HUMAN).//Q92794

F-HEMBB1001910

F-HEMBB1001911

F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15)  
(UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64  
E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTE  
R (FRUIT FLY).//Q24574

F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HO  
MO SAPIENS (HUMAN).//P08547

F-HEMBB1001922

F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED

MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801  
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//  
 0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412  
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.1e-34:63:85/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID T  
 RANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLE  
 EDING) (INCA-WHEAT).//P80450  
 F-HEMBB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1  
 / STRAIN 17).//P10208  
 F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REG  
 ION (O378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062  
 F-HEMBB1001952  
 F-HEMBB1001953  
 F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.7e-11:51:60//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.6e-24:163:42/  
 /HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-35:55:80/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-37:108:75  
 //HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPH  
 AGE ALPHA-3.//P31280  
 F-HEMBB1001988  
 F-HEMBB1001990  
 F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-19:38:73//



HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPH  
 YRA PURPUREA.//P51369  
 F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.6e-12:94:40/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1002009  
 F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION  
 (F67).//1.0:17:47//ESCHERICHIA COLI.//P39395  
 F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.4e-50:1  
 39:55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH).//P29981  
 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3' REGION (ORF3).//0.  
 052:40:42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577  
 F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTE  
 R XYLINUM (ACETOBACTER PASTEURIANUS).//P37697  
 F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55/  
 /HOMO SAPIENS (HUMAN).//P03928  
 F-HEMBB1002049  
 F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CON  
 TAINS: BASIC PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUM  
 AN).//P02812  
 F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56:44//GALLU  
 S GALLUS (CHICKEN).//P17277  
 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP  
 ROTEIN).//0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS:  
 OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E] .//2.4e-07:75:40  
 //BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10269  
 F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.9e-24:63:82  
 //HOMO SAPIENS (HUMAN).//P39191

F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.9  
4:26:42//ZEA MAYS (MAIZE).//P43401

F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NO  
RVEGICUS (RAT).//P56163

F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPH  
YRA PURPUREA.//P51270

F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAG  
O TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC RE  
GION (ORF102).//5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811

F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN CYTOMEGALO  
VIRUS (STRAIN AD169).//P16835

F-HEMBB1002190

F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSI  
NE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN K  
INASE DTK).//1.2e-27:59:100//HOMO SAPIENS (HUMAN).//Q06418

F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOM  
O SAPIENS (HUMAN).//Q99676

F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.6e-21:56:71/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002247

F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.2e-29:93:69/  
/HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:101:67  
//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.  
0:73:28//PARAMECIUM TETRAURELIA.//P15579

F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:26//PL

ASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816  
 F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:36//N  
 YCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBB1002300  
 F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.00011:26:84/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.1e-11:41:85/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REG  
 ION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032  
 F-HEMBB1002340  
 F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REG  
 ION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835  
 F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:  
 63:96//HOMO SAPIENS (HUMAN).//P23919  
 F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0  
 .97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346  
 F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119  
 :25//HOMO SAPIENS (HUMAN).//P12895  
 F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRE  
 CURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09  
 703  
 F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORH  
 ABDITIS ELEGANS.//Q09455  
 F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:1  
 03:32//AQUIFEX AEOLICUS.//066566  
 F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT S  
 HOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626  
 F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUS

CULUS (MOUSE).//P17095  
 F-HEMBB1002415  
 F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-18:55:70/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.  
 //P34692  
 F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:54:75/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:31:64//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01642  
 F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMST  
 ER).//P11414  
 F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.  
 030:182:28//HOMO SAPIENS (HUMAN).//Q15427  
 F-HEMBB1002492  
 F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-08:41:75/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:  
 31:77//HOMO SAPIENS (HUMAN).//P12895  
 F-HEMBB1002509  
 F-HEMBB1002510  
 F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//N  
 YCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRUS B  
 (CVB).//P37990  
 F-HEMBB1002531

F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.1e-36:80:73/  
/HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002545

F-HEMBB1002550//HOMEODOMAIN PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:8  
3:34//MUS MUSCULUS (MOUSE).//P23813

F-HEMBB1002556

F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR  
35 KD SUBUNIT) (U2 SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.  
0e-06:27:77//SUS SCROFA (PIG).//Q29350

F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGG  
PLANT) (AUBERGINE).//P01078

F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3' REGION (ORF1) (FRAGMENT).  
//1.9e-20:90:54//PSEUDOMONAS AERUGINOSA.//P28812

F-HEMBB1002596

F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (  
HUMAN).//O14817

F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCC  
US PYOGENES.//P08089

F-HEMBB1002603

F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162

F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HO  
MO SAPIENS (HUMAN).//P08547

F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//  
HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P20553

F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS T  
UNETANUS (COMMON EUROPEAN SCORPION).//P55902

F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:31:54//BACTERIOPHAGE P4.//P12552

F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779

F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B) (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136

F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879

F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885

F-HEMBB1002686

F-HEMBB1002692

F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13.//P03669

F-HEMBB1002699

F-HEMBB1002702

F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//3.6e-40:180:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212

F-HEMBB1002712

F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000019

F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HOMO SAPIENS (HUMAN).//P49326

F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO  
 RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q04475

F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//B  
 OVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412

F-MAMMA1000045

F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:13  
 8:55//MUS MUSCULUS (MOUSE).//P47226

F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69/  
 /HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORG  
 YIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73/  
 /HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.1  
 6) (CYSTEINE-- TRNA LIGASE) (CYSRS).//6.6e-38:90:51//SCHIZOSACCHAROMYCES  
 POMBE (FISSION YEAST).//Q09860

F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.4e-30:43:86/  
 /HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
 38:17:52//HOMO SAPIENS (HUMAN).//P22531

F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HAL  
 OARCULA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116

F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR  
 VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-MAMMA1000133

F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS J  
 ANNASCHII.//Q58063

F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-  
 3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//

P29798

F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:27//MUS MUSCULUS (MOUSE).//P51125

F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09456

F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463

F-MAMMA1000171

F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643

F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901

F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523

F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1000221

F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379

F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370

F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771

F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3' REGION (ORF2).//0.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470



F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550

F-MAMMA1000266

F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.5e-42:95:84//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28481

F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//HORDEUM VULGARE (BARLEY).//P17991

F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.4e-17:56:76//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324

F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-32:84:58//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM VULGARE (BARLEY).//P17992

F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832

F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658

F-MAMMA1000312

F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337

F-MAMMA1000331

F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMAUTOTROPHICUM.//026117

F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039

F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000360

F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72/  
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71/  
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000385

F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPT  
IONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36/  
/HOMO SAPIENS (HUMAN).//P43489

F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MO  
USE).//P47708

F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//H  
OMO SAPIENS (HUMAN).//P08547

F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5  
.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//  
HOMO SAPIENS (HUMAN).//Q16718

F-MAMMA1000413//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (M  
OUSE).//P11369

F-MAMMA1000414

F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./  
/4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232

F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76/  
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANT

IC COD).//P51902

F-MAMMA1000423

F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//H

OMO SAPIENS (HUMAN).//P39189

F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-

05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58/

/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.3e-25:65:76/

/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584

F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I./

/0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA

ROBUSTA (FRUIT FLY).//Q03296

F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:106:55/

/HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-35:80:68/

/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.8e-24:74:77/

/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (

RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682

F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:

33:54//HUMAN.IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).

//P12506

F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-32:43:83/

/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000516

F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACCINIA VIRUS (STRAIN WR).//P17359

F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CALINECTES SAPIDUS (BLUE CRAB).//P55949

F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF.//0.98:37:35//ESCHERICHIA COLI.//P33939

F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-37:95:76//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//4.1e-07:34:64//HOMO SAPIENS (HUMAN).//P39191

F-MAMMA1000583

F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-28:89:75//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.8e-24:38:71//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.1e-25:74:77//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-18:83:50//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318

F-MAMMA1000616

F-MAMMA1000621

F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K).//0.0045:25:48//HOMO SAPIENS (HUMAN).//P80296

F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00078:79:35//MU

S MUSCULUS (MOUSE).//P05143  
 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN.//1.0:25:28//MAGUARI VIRUS./  
 /P16607  
 F-MAMMA1000664  
 F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-05:186:30//H  
 OMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.6e-06:195:30//M  
 US MUSCULUS (MOUSE).//P05143  
 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//  
 3.8e-28:184:35//AEDES AEGYPTI (YELLOWFEVER MOSQUITO).//P42660  
 F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21).//1.1e-07:55:56//HERPES SIMP  
 LEX VIRUS (TYPE 1 / STRAIN 17).//P04487  
 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-31:97:74/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.31:19:42/  
 /CALLINECTES SAPIDUS (BLUE CRAB).//P55950  
 F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE).//1.6e-05:8  
 8:35//LACTOBACILLUS PENTOSUS.//P21939  
 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL  
 OXIDASE).//0.44:126:30//RATTUS NORVEGICUS (RAT).//P16636  
 F-MAMMA1000718//METALLOTHIONEIN-IIE (MT-2E).//1.0:51:31//ORYCTOLAGUS CUN  
 ICULUS (RABBIT).//P80292  
 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-28:60:71/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.7e-14:63:53//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//1.  
 8e-43:258:43//HOMO SAPIENS (HUMAN).//014647  
 F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.9e-12:76:55//

HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1000733  
 F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN).//2.5e-18:181:39//SACCHAROM  
 YCES CEREVISIAE (BAKER'S YEAST).//P14906  
 F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.  
 //5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115  
 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//6.3e-36:144:4  
 7//HOMO SAPIENS (HUMAN).//P39190  
 F-MAMMA1000746  
 F-MAMMA1000752  
 F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.6e-29:75:72/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-09:59:64/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000775  
 F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-35:99:74/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-19:65:70/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000782  
 F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULU  
 S (MOUSE).//P11260  
 F-MAMMA1000802//MYOSIN IC HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELL  
 ANII (AMOEBE).//P10569  
 F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582  
 F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT./  
 /1.0:30:46//ESCHERICHIA COLI.//P19929  
 F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-28:80:58//  
 HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:36//METHANOB  
 ACTERIUM THERMOAUTOTROPHICUM.//O27540

F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDE  
 UM VULGARE (BARLEY).//P17992

F-MAMMA1000843

F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.  
 43:58:34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895

F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS ELEGA  
 NS.//P34687

F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.  
 00098:149:32//HOMO SAPIENS (HUMAN).//Q15428

F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIOS.//P5  
 5952

F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE HERPESVI  
 RUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968

F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INH  
 IBITOR).//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSE  
 LASMA RHODOSTOMA).//P17494

F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.4e-16:41:68//  
 HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.030:10  
 0:32//HOMO SAPIENS (HUMAN).//P81489

F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.98:43:32  
 //APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272

F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUM  
 AN).//P02814

F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-22:85:71/  
 /HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-38:62:74//

HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BO  
 S TAURUS (BOVINE).//P25508  
 F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0  
 .87:15:60//CAENORHABDITIS ELEGANS.//Q11116  
 F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (I  
 ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RE  
 LATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120)./  
 /5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624  
 F-MAMMA1000905  
 F-MAMMA1000906  
 F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS  
 TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19299  
 F-MAMMA1000921  
 F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-10:49:65//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:54//RE  
 CLINOMONAS AMERICANA.//O21281  
 F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-25:55:69//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-08:36:75/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000943  
 F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (A  
 NTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA  
 NEW GUINEA).//P04930  
 F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.024:37:3



7//ESCHERICHIA COLI.//Q47185  
F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.0e-39:61:78/  
/HOMO SAPIENS (HUMAN).//P39189  
F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0054:29:72//  
HOMO SAPIENS (HUMAN).//P39194  
F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABD  
ITIS ELEGANS.//P35799  
F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HU  
MAN).//P02814  
F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCUL  
US (MOUSE).//P15973  
F-MAMMA1000998  
F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TY  
PE 33.//P06426  
F-MAMMA1001008//PROGASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FR  
AGMENT).//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P0  
3955  
F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.01  
6:61:42//STREPTOMYCES FRADIAE.//P20186  
F-MAMMA1001024  
F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (L  
SH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//2.4e-20:234:29//GALL  
US GALLUS (CHICKEN).//Q90674  
F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-15:52:78/  
/HOMO SAPIENS (HUMAN).//P39193  
F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II).//  
0.53:25:48//RADIANTHUS PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS  
).//P01534  
F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS M

USCULUS (MOUSE).//P15508

F-MAMMA1001050

F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:1  
87:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722

F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1)./  
/1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244

F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//H  
OMO SAPIENS (HUMAN).//P08547

F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//  
HOMO SAPIENS (HUMAN).//P29374

F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//H  
OMO SAPIENS (HUMAN).//P08547

F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:8  
2:71//HOMO SAPIENS (HUMAN).//P01764

F-MAMMA1001082

F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BAR  
R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HO  
MO SAPIENS (HUMAN).//P08547

F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSO  
PHILA MELANOGASTER (FRUIT FLY).//P51521

F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//  
MUS MUSCULUS (MOUSE).//P02463

F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.3e-07:66:45/  
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC RE  
GION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174

F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.

4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201  
 F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00014:36:66//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001145  
 F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953  
 F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.2e-23:53:64//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27  
 ).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272  
 F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.  
 //0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486  
 F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-32:44:86/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (  
 FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466  
 F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15  
 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN)./  
 /P42566  
 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.52:46:32/  
 /CALLINECTES SAPIDUS (BLUE CRAB).//P55950  
 F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.3e-11:82:58/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:67:71//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994  
 F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-37:55:87/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//M  
 YCOBACTERIUM TUBERCULOSIS.//Q10690

F-MAMMA1001243

F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055

F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3' REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774

F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486

F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219:27//HOMO SAPIENS (HUMAN).//P13535

F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259

F-MAMMA1001274//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54//ESCHERICHIA COLI.//P05834

F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:69//HOMO SAPIENS (HUMAN).//Q14681

F-MAMMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29:37//HAEMOPHILUS INFLUENZAE.//P44668

F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9.9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960

F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46

:60//HOMO SAPIENS (HUMAN).//P20931  
 F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)]./2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808  
 F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044  
 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS (HUMAN).//P26651  
 F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927  
 F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33:45//SOLANUM TUBEROSUM (POTATO).//P01082  
 F-MAMMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-30:86:77//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195:92//HOMO SAPIENS (HUMAN).//P02750  
 F-MAMMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-19:55:69//HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841  
 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640  
 F-MAMMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-16:99:51//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/0.0018:23:65//HOMO SAPIENS (HUMAN).//P39190  
 F-MAMMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.7e-22:60:58/

/HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1001442  
 F-MAMMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-23:48:75/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIOPHAGE L  
 5.//Q05245  
 F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS  
 TYPE 2.//P03290  
 F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE)  
 (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623  
 F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO  
 SAPIENS (HUMAN).//P07384  
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES  
 FRADIAE.//P26800  
 F-MAMMA1001510  
 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67  
 :98:31//STREPTOMYCES FRADIAE.//P20186  
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42/  
 /HAEMOPHILUS INFLUENZAE.//P45183  
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS  
 JANNASCHII.//P81308  
 F-MAMMA1001575  
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN  
 CLAWED FROG).//P23330  
 F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:38:55//  
 HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//  
HOMO SAPIENS (HUMAN).//P29279  
F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.  
//0.14:82:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902  
F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO  
SAPIENS (HUMAN).//P52926  
F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-05:24:66/  
/HOMO SAPIENS (HUMAN).//P39195  
F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGAN  
S.//P34804  
F-MAMMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.6e-26:57:78/  
/HOMO SAPIENS (HUMAN).//P39194  
F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (  
HUMAN).//P49910  
F-MAMMA1001635  
F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS  
ACULEATUS (AUSTRALIAN ECHIDNA).//P35311  
F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112  
) (TYROSINE- PROTEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM  
(SLIME MOLD).//P18160  
F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA  
COLI.//P05056  
F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS  
.//P08124  
F-MAMMA1001671  
F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HO  
MO SAPIENS (HUMAN).//P08572  
F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00  
026:147:34//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1001686

F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26

//BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616

F-MAMMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-28:56:69/

/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:39:71//

HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS

PURPURATUS (PURPLE SEA URCHIN).//Q27287

F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS

GALLUS (CHICKEN).//P09653

F-MAMMA1001740

F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42

//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZE

BRAFISH) (ZEBRA DANIO).//Q90270

F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//H

OMO SAPIENS (HUMAN).//P08547

F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//

P34410

F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSO

PHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.94:30:4

3//PSEUDOMONAS PUTIDA.//P25753

F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//4.6e-34:103:5

9//HOMO SAPIENS (HUMAN).//P39191

F-MAMMA1001764

F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGA

LOVIRUS (STRAIN AD169).//P16818



F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-29:97:69/  
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HO  
MO SAPIENS (HUMAN).//P51805

F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-09:55:61//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM  
DISCOIDEUM (SLIME MOLD).//P34143

F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HO  
MO SAPIENS (HUMAN).//P08547

F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-24:69:69//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REG  
ION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042

F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.8e-12:53:69/  
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO  
SAPIENS (HUMAN).//P08547

F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:86:55//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001818

F-MAMMA1001820//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-  
4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
P13238

F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26  
:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271

F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-35:77:88/  
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (

HUMAN).//014754  
 F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0e-19:92:58//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001851  
 F-MAMMA1001854  
 F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:38//CATOST  
 OMUS COMMERSONI (WHITE SUCKER).//P15210  
 F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:1  
 61:27//MYCOPLASMA GENITALIUM.//P47435  
 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS  
 ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE  
 ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S  
 YEAST).//P38911  
 F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:3  
 1//MUS MUSCULUS (MOUSE).//P07978  
 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1)  
 (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157  
 F-MAMMA1001880  
 F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.1e-34:56:83/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-12:44:68/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC RE  
 GION.//0.00013:77:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03525  
 F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.  
 //0.41:106:29//CAENORHABDITIS ELEGANS.//Q09564  
 F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSC  
 ULUS (MOUSE).//Q06666  
 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5' REGION (ORF X) (FRAGMENT).

//1.0:46:28//KLEBSIELLA AEROGENES.//Q08600  
 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:68//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:37//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//Q02722  
 F-MAMMA1002009//PROBABLE E5 PROTEIN.//0.17:56:32//HUMAN PAPILLOMAVIRUS T  
 YPE 31.//P17385  
 F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (   
 PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L P  
 ROTEIN).//1.0:100:31//HOMO SAPIENS (HUMAN).//P29966  
 F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:86:65//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.5e-20:67:58//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//DROSOPH  
 ILA MELANOGASTER (FRUIT FLY).//Q01644  
 F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.19:45:46//HO  
 MO SAPIENS (HUMAN).//P39192  
 F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXO  
 GLUTARATE AMINOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NORVEGICUS (RAT  
 ).//P04694  
 F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.2e-37:70:77/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-08:26:76//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:46//HO  
 MO SAPIENS (HUMAN).//P08547  
 F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:26:46/

/COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P50682  
F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES CER  
EVISIAE (BAKER'S YEAST).//P32583  
F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P20520  
F-MAMMA1002093  
F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00  
079:143:33//STREPTOMYCES FRADIAE.//P20186  
F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:43:34//  
METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//047493  
F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.9e-14:60:68/  
/HOMO SAPIENS (HUMAN).//P39192  
F-MAMMA1002132  
F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-24:69:65//  
HOMO SAPIENS (HUMAN).//P39188  
F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMA  
N).//Q00587  
F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCOPERSIC  
ON ESCULENTUM (TOMATO).//Q00451  
F-MAMMA1002153  
F-MAMMA1002155  
F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34//STRE  
PTOMYCES NIGRESCENS.//P01077  
F-MAMMA1002158  
F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.0e-66  
:157:70//HOMO SAPIENS (HUMAN).//P15880  
F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.5e-25:56:64//  
HOMO SAPIENS (HUMAN).//P39188  
F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE

REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL  
KILLER CELL ENHANCING FACTOR B) (NKEF-B).//9.0e-09:28:100//HOMO SAPIENS  
(HUMAN).//P32119

F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.0023:132:33//HOMO SAPIENS  
(HUMAN).//000268

F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.00032:68:35//  
HOMO SAPIENS (HUMAN).//P02452

F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.0079:22  
4:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-  
2B GDP-GTP EXCHANGE FACTOR).//1.4e-118:151:94//RATTUS NORVEGICUS (RAT)./  
/P70541

F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.028:  
112:33//MUS MUSCULUS (MOUSE).//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.0012:8  
0:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.17:13  
9:28//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOPHILA M  
ELANOGASTER (FRUIT FLY).//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:14:57//  
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65/  
/HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P40414

F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44/

/HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.00011:138:3  
 8//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020  
 F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:144:30/  
 /SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:50//MU  
 S MUSCULUS (MOUSE).//P05143  
 F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .84:65:32//STRUTHIO CAMELUS (OSTRICH).//021405  
 F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-29:61:73//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0001  
 6:70:38//MUS MUSCULUS (MOUSE).//P15265  
 F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.4e-09:84:54/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REG  
 ION (URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084  
 F-MAMMA1002317  
 F-MAMMA1002319//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS (M  
 OUSE).//P11369  
 F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.2e-20:92:57/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36  
 //XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931  
 F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//H  
 OMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:214:31//B  
 OS TAURUS (BOVINE).//P02453

F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMAT  
IA (ROMAN SNAIL) (EDIBLE SNAIL).//P55947

F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.43:26:61//HOM  
O SAPIENS (HUMAN).//P39188

F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOC  
CUS JANNASCHII.//Q57752

F-MAMMA1002352

F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00028:31:80//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.2e-28:87:73/  
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).  
//P11953

F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUIL  
LARDIA THETA (CRYPTOMONAS PHI).//078487

F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:  
43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626

F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.0e-08:45:68//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26/  
/LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DRO  
SOPHILA SIMULANS (FRUIT FLY).//P13729

F-MAMMA1002384

F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REG  
ION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241

F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//  
BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//021003

F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP

. (STRAIN PCC 6803).//P73311  
 F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926  
 F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786  
 F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217  
 F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1002446  
 F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329  
 F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551  
 F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795  
 F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532  
 F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741  
 F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823  
 F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848  
 F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517  
 F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION



GION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571  
 F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHA  
 TIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12  
 :88:44//HOMO SAPIENS (HUMAN).//P47712  
 F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-29:97:71/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER)  
 .//P11414  
 F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-2  
 0-IB).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251  
 F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65  
 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207  
 F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35  
 084  
 F-MAMMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20  
 962  
 F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR I  
 SOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542  
 F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.99:22:77//HO  
 MO SAPIENS (HUMAN).//P39195  
 F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-18:44:70/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS  
 (HUMAN).//P18124  
 F-MAMMA1002603  
 F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMU  
 S AQUATICUS.//007348

F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164

F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINEREA.//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931

F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.4e-05:53:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021

F-MAMMA1002625

F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-19:49:73//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//HOMO SAPIENS (HUMAN).//P12110

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVEGICUS (RAT).//P37285

F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246

F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:25:44//HOMO SAPIENS (HUMAN).//P22532

F-MAMMA1002662

F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-07:54:57//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA

LIGASE) (ACYL- ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P  
27550

F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS  
(BOVINE).//Q28062

F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REG  
ION.//0.094:77:27//BACTERIOPHAGE T4.//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//R  
ATTUS NORVEGICUS (RAT).//P02454

F-MAMMA1002698

F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REG  
ION.//1.2e-28:127:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:14:92//HOMO  
SAPIENS (HUMAN).//P39188

F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.9e-27:52:65/  
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-24:54:75//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002721

F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MO  
USE).//Q04891

F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS T  
ENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305

F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REG  
ION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULF  
OLOBUS VIRUS-LIKE PARTICLE SSV1.//P20198

F-MAMMA1002748

F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-21:56:64//  
HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.7e-32:79:60/  
/HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814

F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE  
(FISSION YEAST).//P41891

F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//  
5.4e-54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-MAMMA1002780

F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS  
(SCORPION).//P40755

F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS FLUO  
RESCENS.//P09815

F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.3e-23:100:59/  
/HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002820//NEUROTOXIN IV (LQQ IV).//1.0:18:50//LEIURUS QUINQUESTRIA  
TUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489

F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.7e-24:55:74/  
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.6e-31:95:73/  
/HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1  
.0:54:37//CAENORHABDITIS ELEGANS.//Q19417

F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.5e-27:99:70/  
/HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.3e-13:65:63/  
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (M

OUSE).//P02798

F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//4.9e-08:119:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37//PAN TROGLODYTES (CHIMPANZEE).//Q35647

F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.8e-10:51:62//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059

F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//012000

F-MAMMA1002880

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-22:180:35//HOMO SAPIENS (HUMAN).//P48060

F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706

F-MAMMA1002887

F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-MAMMA1002892

F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00011:28:75//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730

F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1)./  
/6.5e-24:147:34//HOMO SAPIENS (HUMAN).//P28698

F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.  
7e-11:44:68//MUS MUSCULUS (MOUSE).//Q61147

F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q027  
22

F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e  
-08:152:38//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1002964

F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0057:55:43//  
HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002972//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (  
OCT-T1) (HOMEBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS (  
HUMAN).//Q01851

F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.6e-11:54:68/  
/HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002982

F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REG  
ION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906

F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.6e-09:30:73/  
/HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0071:41:58//  
HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATU  
S ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS  
(RAT).//Q02874

F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGU  
US (YEAST).//P38479

F-MAMMA1003015

F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q1349

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F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//OR

GYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-MAMMA1003031//PROBABLE E4 PROTEIN (E1'E4).//0.14:49:32//HUMAN PAPILLOM

AVIRUS TYPE 6B.//P06459

F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3' REGION (ORF4).//5.

1e-12:112:34//ZYMOMONAS MOBILIS.//066114

F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-07:68:54//

HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//2.8e-39:90:57

//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1003044

F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//B

OS TAURUS (BOVINE).//P19782

F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS T

YPE 6C.//P20969

F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN C

OBRA).//P01415

F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS

PNEUMONIAE.//P35597

F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60

584

F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q0338

1

F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//5.1e-15:44:77

//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE F

ILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333  
 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:40/  
 /SYNECHOCOCCUS ELONGATUS NAEGELI.//P25900  
 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.6  
 7:35:45//GALLUS GALLUS (CHICKEN).//P02467  
 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULU  
 S (MOUSE).//P46735  
 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC RE  
 GION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-MAMMA1003140  
 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHI  
 LA MELANOGASTER (FRUIT FLY).//P08175  
 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II./  
 /4.4e-10:254:30//CAENORHABDITIS ELEGANS.//Q09625  
 F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN).  
 //043236  
 F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC RE  
 GION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
 F-NT2RM1000018  
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41/  
 /CYPRINUS CARPIO (COMMON CARP).//P24948  
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.  
 1.34) (HMG-COA REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN  
 COCKROACH).//P54960  
 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA  
 (MUD CRAB).//P02806  
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84  
 :33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q06521  
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:55//P



LASMODIUM LOPHURAE.//P04929

F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN).//Q02080

F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUMAN).//P02814

F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:40//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P72655

F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162

F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22576

F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//5.7e-07:109:28//NEUROSPORA CRASSA.//P87072

F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276

F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:68:32//SORGHUM VULGARE (SORGHUM).//P24152

F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.82:33:39//BOS TAURUS (BOVINE).//P37359

F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124:91//HOMO SAPIENS (HUMAN).//075380

F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:148:29//HOMO SAPIENS (HUMAN).//P49902

F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.9e-07:109:27//NEUROSPORA CRASSA.//P87072

F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI  
CASE SPAC10F6.02C.//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YE  
AST).//042643

F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:33//CAENORHABDI  
TIS ELEGANS.//P20630

F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.3  
4).//0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013931

F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X./  
/0.0055:98:36//CAENORHABDITIS ELEGANS.//Q11102

F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P2279  
3

F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOM  
ERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-  
PHOSPHATE AMIDOTRANSFERASE) (GFAT).//2.9e-54:153:67//MUS MUSCULUS (MOUS  
E).//P47856

F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA MELANOGA  
STER (FRUIT FLY).//P49028

F-NT2RM1000260

F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS SUBTIL  
IS.//P39574

F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III.  
//8.8e-25:131:45//CAENORHABDITIS ELEGANS.//Q09357

F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE  
D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAU  
RUS (BOVINE).//P39942

F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//0.  
51:145:26//HOMO SAPIENS (HUMAN).//Q13428

F-NT2RM1000314

F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX AEOLICUS

./066433

F-NT2RM1000341

F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5' REGION (ORF55).//0

.95:43:37//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDU

LIS (BLUE MUSSEL).//Q04621

F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPI

ENS (HUMAN).//Q14153

F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC

3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE

PHOSPHATASE 4) (MKP-4).//4.9e-18:113:38//HOMO SAPIENS (HUMAN).//Q99956

F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE

GION.//0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIEN

S (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CU

NICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC

SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI (

FRUIT FLY).//P06351

F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//C

ANIS FAMILIARIS (DOG).//P12064

F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS

CONTORTUS.//P16252

F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).//

/0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO).//Q03211

F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49

//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC RE

GION.//2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS

SCROFA (PIG).//P17403  
 F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//  
 P18395  
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.15:20:50//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCPBP  
 ) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIEN  
 S (HUMAN).//P11684  
 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43636  
 F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)  
 (GIF) (GIFB).//0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713  
 F-NT2RM1000666//COLD SHOCK PROTEIN SCOF.//9.1e-07:67:41//STREPTOMYCES CO  
 ELICOLOR.//P48859  
 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//POR  
 PHYRA PURPUREA.//P51290  
 F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0  
 .27:42:42//KLUYVEROMYCES LACTIS (YEAST).//013475  
 F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:  
 42//HOMO SAPIENS (HUMAN).//P29375  
 F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR  
 (EC 2.1.1.32).//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P15565  
 F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.//0.00  
 13:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26308  
 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:15:60//HOMO  
 SAPIENS (HUMAN).//P02811  
 F-NT2RM1000741//STATHMIN (CLONE X020) (FRAGMENT).//1.0:53:32//XENOPUS LA  
 EVIS (AFRICAN CLAWED FROG).//Q09005

F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3' REGION (ORF2).//1  
 .0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77).//P25049  
 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I.//  
 0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09858  
 F-NT2RM1000770//DXS6673E PROTEIN.//2.0e-38:190:48//HOMO SAPIENS (HUMAN).  
 //Q14202  
 F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.3e-12:14  
 1:30//PODOSPORA ANSERINA.//Q00808  
 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:34:38//DROSOPH  
 ILA MELANOGASTER (FRUIT FLY).//P08175  
 F-NT2RM1000781  
 F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.//7.9e-1  
 1:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28707  
 F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMY  
 LASE INHIBITOR OF MICROBES I).//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS  
 (STREPTOMYCES CORCHORUSII).//P09921  
 F-NT2RM1000811  
 F-NT2RM1000826//UNR PROTEIN.//1.1e-110:144:83//RATTUS NORVEGICUS (RAT)./  
 /P18395  
 F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:38:34//  
 DROSOPHILA SIMULANS (FRUIT FLY).//P50270  
 F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:  
 145:84//CANIS FAMILIARIS (DOG).//P38377  
 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:  
 136:33//RATTUS NORVEGICUS (RAT).//Q63572  
 F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHA  
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P45818  
 F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273  
 F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-)

.//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965  
 F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P40312  
 F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW  
 MOSAIC VIRUS (CYMV).//P16485  
 F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7  
 .7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUB  
 UNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//054888  
 F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:2  
 8//OXYTRICHA FALLAX.//P02583  
 F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA  
 ).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOW  
 FLY).//P42860  
 F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.  
 //1.3e-11:169:28//CAENORHABDITIS ELEGANS.//P46577  
 F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEG  
 ANS.//P08124  
 F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7  
 .1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014180  
 F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REG  
 ION.//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045  
 F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN)  
 .//1.6e-21:211:31//GALLUS GALLUS (CHICKEN).//P30997  
 F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3  
 .2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469

F-NT2RM1001044

F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490

F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPE RSICON ESCULENTUM (TOMATO).//Q43513

F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174

F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2.//P03291

F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.5e-19:75:54//HOMO SAPIENS (HUMAN).//P39195

F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e-42:200:38//HOMO SAPIENS (HUMAN).//P51522

F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5333

1

F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-05:157:35//STREPTOMYCES FRADIAE.//P20186

F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOSTAURUS (BOVINE).//P02313

F-NT2RM1001115

F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//P10496

F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.76:45:35//LEISHMANIA

ANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940  
 F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2  
 .7.7.6) (RNA POLYMERASE III SUBUNIT 2).//3.9e-87:238:65//DROSOPHILA MELA  
 NOGASTER (FRUIT FLY).//P25167  
 F-NT2RM2000030//TOXINS 1 AND 2.//0.98:21:42//TRIMERESURUS WAGLERI (WAGLE  
 R'S PIT VIPER) (TROPIDOLAEMUS WAGLERI).//P24335  
 F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00059:53:49//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.  
 0:68:26//HOMO SAPIENS (HUMAN).//P22532  
 F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC R  
 EGION.//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38748  
 F-NT2RM2000093//OVARY MATURATING PARSIN (OMP).//1.0:26:38//LOCUSTA MIGRA  
 TORIA (MIGRATORY LOCUST).//P80045  
 F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//3  
 .3e-09:56:35//CAENORHABDITIS ELEGANS.//Q11096  
 F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC  
 2.7.1.37) (PKA C-ALPHA).//3.1e-35:77:96//MUS MUSCULUS (MOUSE).//P0513  
 2  
 F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4  
 .17) (PDEASE REGA).//3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOL  
 D).//Q23917  
 F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS).//0.019:148:25//COTTO  
 NTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV).//P5189  
 4  
 F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00032:111:32//M  
 US MUSCULUS (MOUSE).//P05143  
 F-nnnnnnnnnnnnn//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.046:59:33//LYCOP  
 ERSICON ESCULENTUM (TOMATO).//Q43512



F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.054:46:34//RATTUS NORVEGICUS (RAT).//P08699

F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6).//0.27:112:33//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).//P29128

F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-22:191:35//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I.//5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013868

F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE).//0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56129

F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11.//0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P22698

F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.3e-16:203:30//HOMO SAPIENS (HUMAN).//P11274

F-NT2RM2000368//DEK PROTEIN.//0.00027:100:32//HOMO SAPIENS (HUMAN).//P35659

F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE).//6.8e-36:170:47//ESCHERICHIA COLI.//P05055

F-NT2RM2000374//NODAL PRECURSOR.//1.1e-32:64:95//MUS MUSCULUS (MOUSE).//P43021

F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180.//0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC

INTERMEDIATE COMPONENT).//1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKE  
R' S YEAST).//P32802

F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.032:105:30//HOMO  
SAPIENS (HUMAN).//P51805

F-NT2RM2000420//METALLOTHIONEIN (MT).//0.88:42:38//PLEURONECTES PLATESSA  
(PLAICE).//P07216

F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//2.0e-  
117:237:87//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC RE  
GION.//1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P36113

F-NT2RM2000469//70 KD ANTIGEN.//0.050:207:23//SHIGELLA FLEXNERI.//P18010

F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.022:25:44//HOM  
O SAPIENS (HUMAN).//P02811

F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0037:17:58//DROS  
OPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//1.7e-22:195:27  
//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042908

F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT).//3.6e-05:67:29//DIC  
TYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III./  
/8.4e-33:214:38//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-09:133:36/  
/HOMO SAPIENS (HUMAN).//P56524

F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F).//2.2e-60:244  
:51//HOMO SAPIENS (HUMAN).//P23229

F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.3e-09:192:34//M  
US MUSCULUS (MOUSE).//P05143

F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.0e-08:43:72//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:111:34//HOMO SAPIENS (HUMAN).//Q15427

F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO SAPIENS (HUMAN).//P56524

F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO SAPIENS (HUMAN).//P02811

F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.MMUI).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864

F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP).//P81014

F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197

F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730

F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129

F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONORRHOEAE.//P11910

F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.//Q57694

F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P36610

F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS

./P05647

F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P32391

F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022:174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013695

F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:246:74//HOMO SAPIENS (HUMAN).//P28160

F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION.//8.5e-51:212:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38144

F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.0e-41:125:53//HOMO SAPIENS (HUMAN).//P39189

F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1.1e-128:291:89//RATTUS NORVEGICUS (RAT).//P23514

F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//P49918

F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III.//2.5e-49:273:39//CAENORHABDITIS ELEGANS.//P30646

F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P16884

F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//6.3e-44:216:43//CAENORHABDITIS ELEGANS.//P41879

F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RAT).//P09951

F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MUSCULUS (MOUSE).//Q60809

F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//3.4e-13:171:30//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475

F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//CAENORHABDITIS ELEGANS.//P34681

F-NT2RM2001152

F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:42:40//GALLUS GALLUS (CHICKEN).//P32018

F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P5381

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F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101

F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP 10).//1.3e-13:183:32//RATTUS NORVEGICUS (RAT).//P97924

F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT).//P13264

F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION.//0.00019:177:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945

F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN

PEA).//P14594  
 F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109  
 :207:98//MUS MUSCULUS (MOUSE).//P53995  
 F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
 16:22:40//HOMO SAPIENS (HUMAN).//P22531  
 F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (F  
 RUIT FLY).//P14199  
 F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RM2001319  
 F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584  
 F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:15  
 9:27//PODOSPORA ANSERINA.//Q00808  
 F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)  
 .//1.0:27:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623  
 F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUB  
 SP. THIOSPHAERA PANTOTROPHA).//Q56348  
 F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-  
 1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON  
 UNICUSPUS (SILVER LAMPREY).//Q91062  
 F-NT2RM2001420  
 F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4  
 e-41:140:59//HOMO SAPIENS (HUMAN).//Q00839  
 F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)  
 (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LE  
 UKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG)./  
 /3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825  
 F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS  
 .//P17656

F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III./  
/6.7e-47:190:42//CAENORHABDITIS ELEGANS.//Q09316

F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//  
EUPLOTES CRASSUS.//Q06184

F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REG  
ION.//8.5e-18:91:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//3.9e-35:212:41//HOMO SAPIENS (HUMAN).//P19474

F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160

F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06  
:115:32//ZEA MAYS (MAIZE).//P14918

F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
//0.033:156:23//HOMO SAPIENS (HUMAN).//P26371

F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249  
:82//HOMO SAPIENS (HUMAN).//P29375

F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.2e-97:  
192:100//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00068:145:  
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEM  
BRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT  
).//P52591

F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR  
VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:  
29:68//HOMO SAPIENS (HUMAN).//P00387

F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:  
132:100//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAR

OMYCES CEREVISIAE (BAKER'S YEAST).//P11075  
 F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM  
 (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399  
 F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//Q06706  
 F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. C  
 AMPESTRIS).//034261  
 F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (HUMAN).//Q15697  
 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.  
 //1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857  
 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//1.0  
 :184:21//METHANOCOCCUS JANNASCHII.//Q57695  
 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)  
 .//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399  
 F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REG  
 ION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966  
 F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.9e-41:60:81/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI  
 ON.//9.8e-16:126:38//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059  
 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAFII-30) (TAFII30).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962  
 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P5054



F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.5e-33:95:75/  
/HOMO SAPIENS (HUMAN).//P39195

F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE  
GION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
//P47179

F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77:37  
//BACILLUS SUBTILIS.//P39217

F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BO  
VINE).//P01154

F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//  
P50781

F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (   
EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PR  
OTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGA  
NS.//Q09931

F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS  
(GUINEA PIG).//P47969

F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAP  
IENS (HUMAN).//Q92609

F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:  
119:99//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALO  
VIRUS (STRAIN AD169).//P16761

F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (   
HUMAN).//P52742

F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP  
-MANNOSE-1- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE  
).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOME

GALOVIRUS (STRAIN AD169).//P16818  
 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871  
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742  
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093  
 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706  
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//033793  
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963  
 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//014647  
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293  
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723  
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800  
 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798  
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REG

ION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582  
 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCU  
 S JANNASCHII.//006917  
 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS  
 (MOUSE).//Q03350  
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAE  
 NORHABDITIS ELEGANS.//Q21184  
 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27  
 :216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320  
 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLE  
 NSIS (BUFFALO LEECH).//P81492  
 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-  
 8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154  
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (  
 HUMAN).//P02814  
 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-  
 24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838  
 F-NT2RM2001997  
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIE  
 S VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//Q12034  
 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILU  
 S INFLUENZAE.//P71353  
 F-NT2RM2002030//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOM  
 ERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-  
 PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOU  
 SE).//P47856  
 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIE

NS (HUMAN).//P35326  
 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.01  
 2:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878  
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRN  
 P X) (CBP).//1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990  
 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R  
 EGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHA  
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P45818  
 F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TR  
 KC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEG  
 ICUS (RAT).//Q03351  
 F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
 0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACH  
 YDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805  
 F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0  
 .0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488  
 F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39/  
 /BOS TAURUS (BOVINE).//P25508  
 F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF  
 -Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2  
 .9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210  
 F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2  
 .7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELA  
 NOGASTER (FRUIT FLY).//P25167  
 F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.99:72:3  
 1//MUS MUSCULUS (MOUSE).//P15091  
 F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE

(BAKER'S YEAST).//P36146

F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS NORVEGICUS (RAT).//P13941

F-NT2RM4000061

F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE).//070133

F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221

F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741

F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874

F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639

F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174

F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469

F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783

F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587

F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162

F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF3).//0.

52:42:40//BACILLUS LICHENIFORMIS.//P22754  
 F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLL  
 AGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282  
 F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT)  
 .//P06599  
 F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P10962  
 F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (F  
 ISSION YEAST).//P41891  
 F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO  
 SAPIENS (HUMAN).//P51805  
 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27/  
 /BALAENOPTERA PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947  
 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MU  
 S MUSCULUS (MOUSE).//P05143  
 F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.1e-38:70:70//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209  
 :94//HOMO SAPIENS (HUMAN).//Q04726  
 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTE  
 LIUM DISCOIDEUM (SLIME MOLD).//Q04503  
 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION  
 .//0.91:73:28//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV  
 ).//P41703  
 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAE  
 NORHABDITIS ELEGANS.//P54813  
 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO C  
 ALIFORNICA (PACIFIC ELECTRIC RAY).//P56101  
 F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:

208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371  
 F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIR  
 US (STMV).//P17574  
 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPESVIRUS SA  
 IMIRI (STRAIN 11).//Q01042  
 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGI  
 ON.//0.54:46:36//BACTERIOPHAGE RB69.//064300  
 F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI  
 .//P16918  
 F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC  
 REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P436  
 16  
 F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.13:33:  
 48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820  
 F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:29//SACCHAR  
 OMYCES CEREVISIAE (BAKER'S YEAST).//Q99189  
 F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.1e-25:46:80/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS CONTORT  
 US.//P16253  
 F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I  
 .//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297  
 F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALB  
 ICANS (YEAST).//P87185  
 F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GA  
 LLUS GALLUS (CHICKEN).//P15988  
 F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RNA POLYMERASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES  
 POMBE (FISSION YEAST).//P36594

F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:31//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q37708

F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPINACIA OLERACEA (SPINACH).//P08974

F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO SAPIENS (HUMAN).//Q14929

F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01049

F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614

F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26].//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISY) (HIV-2).//P12450

F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//CAENORHABDITIS ELEGANS.//P34284

F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO SAPIENS (HUMAN).//Q14247

F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963

F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P



27550

F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHO  
CYSTIS SP. (STRAIN PCC 6803).//P74168

F-NT2RM4000689

F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC  
-A.12).//0.26:45:33//BOMBYX MORI (SILK MOTH).//P05687

F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25  
//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P53364

F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3  
(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING P  
ROTEASE) (DEUBIQUITINATING ENZYME).//2.2e-82:152:63//CAENORHABDITIS ELEG  
ANS.//P34547

F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROS  
OPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSC  
ULUS (MOUSE).//Q06666

F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT).//7.2e  
-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18715

F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHOR  
T-NOSED BANDICOOT).//P42136

F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT  
) .//5.2e-77:246:52//MUS MUSCULUS (MOUSE).//P10076

F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OV  
IS ARIES (SHEEP).//Q02958

F-NT2RM4000778

F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:4  
5//VOLVOX CARTERI.//P21997

F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BM  
P-1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063

F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCOLINESTERASE).//7.4e-41:271:36//HOMO SAPIENS (HUMAN).//P06276

F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ESCHERICHIA COLI.//P15005

F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577

F-NT2RM4000820

F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCUS JANNASCHII.//Q58536

F-NT2RM4000848//BRAIN-SPECIFIC HOMEODOMAIN/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208

F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HUMAN).//P35325

F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//P39194

F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38903

F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION.//3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572.//0.090:68:29//METHANOCOCCUS JANNASCHII.//Q57992

F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC).//0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID).//P46825

F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN R

LC).//1.2e-07:25:96//HOMO SAPIENS (HUMAN).//P19105  
F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC  
ZINC FINGER PROTEIN).//1.4e-56:253:46//MUS MUSCULUS (MOUSE).//P17141  
F-NT2RM4001002  
F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT  
PROTEIN P12; CORE SHELL PROTEIN P30].//0.25:101:31//FBR MURINE OSTEOSARC  
OMA VIRUS.//P29175  
F-NT2RM4001032//CUTICLE COLLAGEN 2.//2.6e-07:130:39//CAENORHABDITIS ELEG  
ANS.//P17656  
F-NT2RM4001047//MO25 PROTEIN.//5.6e-107:252:80//MUS MUSCULUS (MOUSE).//Q  
06138  
F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.0e-109  
:209:94//CANIS FAMILIARIS (DOG).//P38377  
F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTE  
RGENIC REGION.//0.57:95:30//ESCHERICHIA COLI.//P39376  
F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.  
//2.5e-47:231:47//CAENORHABDITIS ELEGANS.//Q09531  
F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II./  
/1.3e-08:243:23//CAENORHABDITIS ELEGANS.//Q09417  
F-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//7.1e-13:103:38//BRACHYDANIO RER  
IO (ZEBRAFISH) (ZEBRA DANIO).//Q01704  
F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).//0.26:96:34//HO  
MO SAPIENS (HUMAN).//P17600  
F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//3.6e-103:201:91//BOS TAU  
RUS (BOVINE).//Q27969  
F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRA  
GMENTS).//1.0:33:36//BRASSICA OLERACEA (CAULIFLOWER).//P48438  
F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT.//0.44:158:27//MYCOP  
LASMA GENITALIUM.//P47318

F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C).//0.99:44:43//ASTROTIA STOKES  
SI (STOKES' S SEA SNAKE) (DSTEIRA STOKESI).//P01381

F-NT2RM4001200//ZINC FINGER PROTEIN 135.//2.2e-82:245:59//HOMO SAPIENS (HUMAN).//P52742

F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P53214

F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.0096:182:34//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-21:221:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RM4001256//CBP3 PROTEIN PRECURSOR.//0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P21560

F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00031:132:39//STREPTOMYCES FRADIAE.//P20186

F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.048:132:28//HOMO SAPIENS (HUMAN).//P02812

F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54676

F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//1.7e-10:185:30//RATTUS NORVEGICUS (RAT).//P08503

F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.5e-08:197:26//MUS MUSCULUS (MOUSE).//P52734

F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//7.7e-14:82:36//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P32626

F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P53

742

F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION.//0.067:111:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04511

F-NT2RM4001371

F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.0e-08:82:39//PLASMODIUM LOPHURAE.//P04929

F-NT2RM4001384

F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P5090

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F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN).//Q13360

F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//P39192

F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425

F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461

F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN).//P52737

F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//P23246

F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929

F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

F-NT2RM4001557

F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919

F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775

F-NT2RM4001582

F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14737

F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221

F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT).//P37199

F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024

F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368

F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS

GALLUS (CHICKEN).//P17277

F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//  
0.29:90:32//HOMO SAPIENS (HUMAN).//P17252

F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REG  
ION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339

F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORH  
ABDITIS ELEGANS.//P52819

F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//  
HOMO SAPIENS (HUMAN).//Q15054

F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPI  
ENS (HUMAN).//Q14141

F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT  
).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342

F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III./  
/1.1e-05:90:33//CAENORHABDITIS ELEGANS.//P34284

F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039

F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VI  
RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03211

F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO  
SAPIENS (HUMAN).//P29400

F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-  
).//5.1e-113:277:79//HOMO SAPIENS (HUMAN).//P27448

F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULU  
S (MOUSE).//P46735

F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169  
:39//MUS MUSCULUS (MOUSE).//P55200

F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON R

HODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397  
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE R  
 ECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULU  
 S (MOUSE).//Q61549  
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CER  
 EBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684  
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e  
 -81:253:59//HOMO SAPIENS (HUMAN).//P51523  
 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:1  
 76:30//NEPHILA CLAVIPES (ORB SPIDER).//P46804  
 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HU  
 MAN).//P02814  
 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//  
 0.98:35:42//CAENORHABDITIS ELEGANS.//Q11104  
 F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REG  
 ION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722  
 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN A  
 NTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P8737  
 7  
 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORH  
 ABDITIS ELEGANS.//P36609  
 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE  
 GION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST  
 ).//P47179  
 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (M  
 OUSE-EAR CRESS).//P93746  
 F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAP  
 IENS (HUMAN), RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14  
 793



F-NT2RM4001922  
 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5  
 e-45:167:53//CAENORHABDITIS ELEGANS.//Q09226  
 F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DI  
 SCOIDEUM (SLIME MOLD).//P54681  
 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.  
 32:31:48//HOMO SAPIENS (HUMAN).//P78415  
 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.2e-43:56:85/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA  
 GORILLA (LOWLAND GORILLA).//P20758  
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4  
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//H  
 OMO SAPIENS (HUMAN).//P04280  
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e  
 -21:103:51//HOMO SAPIENS (HUMAN).//P51523  
 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSC  
 ULUS (MOUSE).//P15974  
 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PRO  
 TEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180  
 F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256  
 F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM  
 DISCOIDEUM (SLIME MOLD).//P14328  
 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.7  
 8:132:25//HOMO SAPIENS (HUMAN).//P98171  
 F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS:  
 LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//  
 0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498

F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI B  
RUCI.//P14044

F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P0  
8105

F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA  
LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)  
.//P36419

F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLU  
S SP. (STRAIN NS-129).//P23342

F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:7  
1//HOMO SAPIENS (HUMAN).//Q93074

F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-15:51:70//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RM4002073//ELASTIN PRECURSOR (TROPOLASTIN).//4.9e-05:88:36//HOMO S  
APIENS (HUMAN).//P15502

F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOU  
S NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB  
-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599

F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULU  
S (MOUSE).//P33174

F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (  
FRAGMENT).//0.91:49:32//PARACOCUS DENITRIFICANS.//P29969

F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22/  
/DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371

F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//P24014

F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGA

STER (FRUIT FLY).//P49028  
 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491  
 F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590  
 F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817  
 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805  
 F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803  
 F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565  
 F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809  
 F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (MOUSE).//P97805  
 F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251  
 F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656  
 F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288  
 F-NT2RM4002281  
 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
 F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556  
 F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT).//0.56:43:39//BACILLUS CALDOLYTICUS.//P42832

F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BO  
S TAURUS (BOVINE).//P02313

F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III).//0.67:34:38//MYTILUS  
EDULIS (BLUE MUSSEL).//P80248

F-NT2RM4002344//METALLOTHIONEIN-I (MT-I).//0.84:41:31//MUS MUSCULUS (MOU  
SE).//P02802

F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR./  
/0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387

F-NT2RM4002374//5E5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q  
63003

F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.13:17:88//HO  
MO SAPIENS (HUMAN).//P39193

F-NT2RM4002390

F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PR  
OTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074

F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTRIX SOEHNGE  
NII.//P27095

F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.7e-15:41:95/  
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RM4002446//CRYPTDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C).//0.0058  
:24:50//MUS MUSCULUS (MOUSE).//P17534

F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II).//0.83:48:37//MYTILUS E  
DULIS (BLUE MUSSEL).//P80247

F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.9e-07:52:63/  
/HOMO SAPIENS (HUMAN).//P39192

F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.92:43:30//HORDEU  
M VULGARE (BARLEY).//P17992

F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIA

NA SYLVESTRIS (WOOD TOBACCO).//P46942  
 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W.//8.8e-26:123:49//S  
 ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12514  
 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR.//0.17:126:27//DROSOP  
 HILA MIRANDA (FRUIT FLY).//P91627  
 F-NT2RM4002499//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-34:92:80/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RM4002504//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-19:55:83/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2.//3.0e-07:193:27//ARABIDOPSIS  
 THALIANA (MOUSE-EAR CRESS).//O22468  
 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN.//0.97:19:47//AEROMONAS SOB  
 RIA.//P09165  
 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32  
 ).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25348  
 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55  
 :204:50//MUS MUSCULUS (MOUSE).//Q60714  
 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:16:62//  
 ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852  
 F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REG  
 ION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032  
 F-NT2RM4002571//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.  
 41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI  
 DE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124:47//HO  
 MO SAPIENS (HUMAN).//Q10472  
 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGI  
 ON.//0.95:36:38//BACILLUS SUBTILIS.//P37509  
 F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS EL  
 EGANS.//P54815

F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA  
LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//  
P73851

F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROS  
OPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENT  
ER (BRAZILIAN ARMED SPIDER).//P17727

F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC RE  
GION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359

F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGI  
ON.//0.16:44:40//ESCHERICHIA COLI.//P22847

F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-  
06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:1  
35:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254

F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT)./  
/1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981

F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:2  
4//MYXOCOCCUS XANTHUS.//P36774

F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//  
MUS MUSCULUS (MOUSE).//P51859

F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA  
(PLAICE).//P07216

F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORAB  
IES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045  
 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR  
 OID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485  
 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOC  
 CUS JANNASCHII.//Q58536  
 F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALL  
 IDUM.//083338  
 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICI  
 NG FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), A  
 ND MUS MUSCULUS (MOUSE).//P23152  
 F-NT2RP1000324  
 F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//  
 1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599  
 F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32447  
 F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:  
 119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343  
 F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGME  
 NT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327  
 F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3' REGION.//7.9  
 e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744  
 F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.  
 2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./  
 /1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157  
 F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESU  
 LFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137  
 F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-  
 131:230:97//RATTUS NORVEGICUS (RAT).//P55161

F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779

F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257

F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P17624

F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580

F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207

F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5' REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194

F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068

F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

F-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367



F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48  
:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SA  
PIENS (HUMAN).//P04275

F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESAT  
URASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOC  
IATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNI  
T) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)./  
/4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE  
GION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)  
.//P47179

F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO  
SAPIENS (HUMAN).//Q07092

F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0024:19:94//  
HOMO SAPIENS (HUMAN).//P39193

F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III./  
/2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:12  
8:93//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIEN  
S (HUMAN).//000268

F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR I  
SOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542

F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5.//0.024:24:45//SACCHAR  
OMYCES CEREVISIAE (BAKER'S YEAST).//P41902

F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSO

R (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C)  
 ) [CONTAINS: PEPTIDE P-C] ./0.040:82:36//HOMO SAPIENS (HUMAN).//P02810  
 F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION  
 ./2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201  
 F-NT2RP1000767//PSEUDOMONAPEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INS  
 ENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101)  
 ./P42790  
 F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTI  
 C LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMO  
 SOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732  
 F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL P  
 ROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SUS SCROFA (PI  
 G).//P35323  
 F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPA  
 SE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3  
 .1e-37:89:64//HOMO SAPIENS (HUMAN).//Q07960  
 F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.3  
 2:29:48//HOMO SAPIENS (HUMAN).//P22531  
 F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202  
 :68//RATTUS NORVEGICUS (RAT).//P70473  
 F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1  
 .0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691  
 F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIE  
 NS (HUMAN).//P35326  
 F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHIL  
 A SALTANS (FRUIT FLY).//Q04536  
 F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)  
 (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUS  
 CULUS (MOUSE).//035566

F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHARO  
MYCES CEREVISIAE (BAKER'S YEAST).//Q02336

F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.  
//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531

F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENI  
C REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40  
010

F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CER  
EVISIAE (BAKER'S YEAST).//P32583

F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HO  
MO SAPIENS (HUMAN).//Q02817

F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//OR  
GYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341

F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U  
BIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6  
e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICU  
S (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669

F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENI  
C REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P4  
0010

F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPR  
K).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321

F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (  
HUMAN).//P19338

F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (  
ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIR  
IDIS.//P04123

F-NT2RP1000988

F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638

F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012

F-NT2RP1001014

F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295

F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826).//P40873

F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218

F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS (HUMAN).//P35326

F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMAN).//P25800

F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT).//Q02874

F-NT2RP1001185

F-NT2RP1001199//NEUROTOXIN I.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BAR K SCORPION).//P01491

F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS (HUMAN).//O00292

F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P1880

F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926

F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110

F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131

F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286

F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0

:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993  
 F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
 //0.053:37:37//OVIS ARIES (SHEEP).//P26372  
 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISI  
 AE (BAKER'S YEAST).//P25382  
 F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOC  
 CUS JANNASCHII.//Q57732  
 F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC R  
 EGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457  
 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNI  
 T C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOM  
 O SAPIENS (HUMAN).//P25789  
 F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS TH  
 ALIANA (MOUSE-EAR CRESS).//Q08891  
 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6  
 .3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803  
 F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEI  
 N CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397  
 F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BE  
 TA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758  
 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III./  
 /9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506  
 F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q033  
 81  
 F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIEN  
 S (HUMAN).//P35326  
 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (  
 HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36)  
 ) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIA  
 A0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q067  
 30

F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA  
 GMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLG  
 US MONKEY).//P50665

F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO  
 SAPIENS (HUMAN).//Q07815

F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAP  
 IENS (HUMAN).//P04281

F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP.  
 THERMOPHILUS).//Q56237

F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORM  
 ONE III) (GNRH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCH  
 US MASOU (CHERRY SALMON) (MASU SALMON).//P30973

F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3  
 .48) (R-PTP- EPSILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446

F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:40/  
 /SALMO SALAR (ATLANTIC SALMON).//P09637

F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPIN  
 E).//P01328

F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:40//DR  
 OSOPHILA MELANOGASTER (FRUIT FLY).//P51022

F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:40  
 //HOMO SAPIENS (HUMAN).//P09234

F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).  
 //P30034

F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245

F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:47//HAEMOPHILUS INFLUENZAE.//P43953

F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P32510

F-NT2RP2000098

F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.4e-09:50:70//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//HOMO SAPIENS (HUMAN).//P42768

F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:32//DESULFOVIBRIO VULGARIS (STRAIN HILDENBOROUGH).//P33391

F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.5e-23:94:47//HOMO SAPIENS (HUMAN).//O14646

F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.6e-10:82:39//HOMO SAPIENS (HUMAN).//Q15427

F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA MALAYI.//Q27450

F-NT2RP2000157//MLO2 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09329

F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS EL EGANS.//Q17632

F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC RE



GION.//0.99:62:25//BACILLUS SUBTILIS.//P54499

F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SP  
ECIFIC PROTEIN NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//002675

F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33/  
/MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949

F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURS  
OR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)  
.//0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54  
463

F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:57//DROSO  
PHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:32//CAENO  
RHABDITIS ELEGANS.//Q09455

F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:38/  
/OVIS ARIES (SHEEP).//002761

F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR)  
(CCK-BR).//0.34:53:43//CANIS FAMILIARIS (DOG).//P30552

F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRA  
GMENT).//0.019:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-NT2RP2000248//OVOMUCOID (FRAGMENT).//0.88:18:55//POLYPLECTRON EMPHANUM  
(PALAWAN PEACOCK-PHEASANT).//P52250

F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:37//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556

F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.081:217:28//DICTYO  
STELIUM DISCOIDEUM (SLIME MOLD).//P08799

F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:80:57//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//0.082:22:45//CLOVER YELLOW  
MOSAIC VIRUS (CYMV).//P16485  
F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III./  
/0.39:38:34//CAENORHABDITIS ELEGANS.//P34535  
F-NT2RP2000288  
F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGI  
ON.//0.40:38:42//ESCHERICHIA COLI.//P22847  
F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)  
.//2.3e-62:206:47//HOMO SAPIENS (HUMAN).//Q03923  
F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//0.55:81:40//CAENORHABDIT  
IS ELEGANS.//P20630  
F-NT2RP2000310//RUBREDOXIN (RD).//0.13:43:41//TREPONEMA PALLIDUM.//08395  
6  
F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//  
GADUS MORHUA (ATLANTIC COD).//P15996  
F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REG  
ION.//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313  
F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (  
AK3).//1.8e-91:155:92//BOS TAURUS (BOVINE).//P08760  
F-NT2RP2000337//PROTEIN A54.//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AN  
D VACCINIA VIRUS (STRAIN COPENHAGEN).//P21072  
F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.  
//9.7e-13:114:42//MUS MUSCULUS (MOUSE).//P17564  
F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT. INHIBITOR).//0.98:47:34//MUS  
MUSCULUS (MOUSE).//Q09098  
F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//0.66:57:36//AIPYSURUS LAE  
VIS (OLIVE SEA SNAKE).//P19960  
F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//1.  
0e-27:96:67//HOMO SAPIENS (HUMAN).//P52597

F-NT2RP2000420//ZINC FINGER PROTEIN 191.//0.16:47:38//HOMO SAPIENS (HUMAN).//014754

F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

F-NT2RP2000438//TUBULIN GAMMA CHAIN.//0.86:190:27//RETICULOMYXA FILOSA.//P54405

F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN.//3.7e-13:140:42//HOMO SAPIENS (HUMAN).//P22059

F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//1.0:45:35//HOMO SAPIENS (HUMAN).//Q16612

F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.062:25:68//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2000503

F-NT2RP2000510//TOXIN IV-5.//1.0:51:33//TITYUS BAHIENSIS (BRAZILIAN SCORPION).//P56608

F-NT2RP2000516//SLYX PROTEIN.//1.0:52:32//ESCHERICHIA COLI.//P30857

F-NT2RP2000523//PHORBOLIN I (FRAGMENTS).//1.4e-06:36:47//HOMO SAPIENS (HUMAN).//P31941

F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III).//0.93:119:26//TRITICUM AESTIVUM (WHEAT).//P04723

F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.056:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934

F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257

F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//

/P08154

F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE)  
(URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607

F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MER  
OZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3  
D7).//P50498

F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00085:38:68//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-17:55:74//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA  
LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//083950

F-NT2RP2000715

F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPOR  
A CRASSA.//P10713

F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00027:31:74//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC  
7120).//P12623

F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLA  
SMA PNEUMONIAE.//P75219

F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e  
-07:133:31//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ES  
CULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083

F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III./  
/3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565

F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCUL  
US (MOUSE).//P21107

F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133  
:26//MUS MUSCULUS (MOUSE).//P27671

F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//  
HOMO SAPIENS (HUMAN).//Q92633

F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:4  
1//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAE  
VIS (AFRICAN CLAWED FROG).//P24793

F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:1  
99:94//HOMO SAPIENS (HUMAN).//O60841

F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHOND  
ROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481

F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43  
244

F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDEN  
T RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MU  
SCULUS (MOUSE).//Q05921

F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).  
//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956

F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42/  
/HOMO SAPIENS (HUMAN).//P53992

F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS  
GALLUS (CHICKEN).//P53352

F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MO  
USE-EAR CRESS).//P93746

F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REG  
ION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159

F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//ANDRO  
CTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P21150

F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.2e-33:65:81/  
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL L  
EECH).//P80302

F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-24:85:65/  
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR  
(BTCI).//0.41:50:32//VIGNA UNGUICULATA (COWPEA).//P17734

F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5)  
(PNP/PMP OXIDASE) (FPRA PROTEIN).//6.2e-18:64:48//MYXOCOCCUS XANTHUS.//P  
21159

F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICUS (RAT  
).//P50232

F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVEGICUS  
(RAT).//P02803

F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.5e-11:61:63/  
/HOMO SAPIENS (HUMAN).//P39195

F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-47:155:5  
8//MUS MUSCULUS (MOUSE).//P41230

F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:39//BO  
S TAURUS (BOVINE).//P25508

F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-13:81:59//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0  
.0071:77:33//RATTUS NORVEGICUS (RAT).//P20468

F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING C  
OFACTOR B).//1.0:36:41//HOMO SAPIENS (HUMAN).//Q99426

F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPIENS (H  
UMAN).//P52743

F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//1.0:95:26//CAPRA HIRCUS (GOAT).//Q36346

F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40486

F-NT2RP2001226//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSCULUS (MOUSE).//P47708

F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//HOMO SAPIENS (HUMAN).//P16415

F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05:230:21//HOMO SAPIENS (HUMAN).//Q15431

F-NT2RP2001268//HOMEBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS EL EGANS.//Q23175

F-NT2RP2001277

F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCULUS (MOUSE).//P28663

F-NT2RP2001295

F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P50426

F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829

F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426

F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.5e-19:66:62//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL).//Q04621

F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSH1IID)

(FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003  
 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1)  
 .//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470  
 F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3.//0.0080:82:3  
 2//OVIS ARIES (SHEEP).//P02441  
 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//D  
 ROSOPHILA MELANOGASTER (FRUIT FLY).//P39769  
 F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRIC  
 ETUS AURATUS (GOLDEN HAMSTER).//P37883  
 F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4  
 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.00018:113:38//  
 HOMO SAPIENS (HUMAN).//P04280  
 F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION  
 (ORF A).//0.90:23:43//BACTERIOPHAGE T4.//P17307  
 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-11:38:68//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55)  
 (LIC-2).//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698  
 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN  
 -1) (KCIP-1).//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35214  
 F-NT2RP2001445  
 F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
 SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS (BOVINE).//Q  
 10568  
 F-NT2RP2001450  
 F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1).//1.0:25:40//BUNGARUS  
 FASCIATUS (BANDED KRAIT).//P10808  
 F-NT2RP2001506  
 F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.



//0.49:124:29//CAENORHABDITIS ELEGANS.//P34681  
 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL  
 (CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//P29377  
 F-NT2RP2001526  
 F-NT2RP2001536//METALLOTHIONEIN-I (MT-1).//1.0:19:42//COLUMBA LIVIA (DOM  
 ESTIC PIGEON).//P15786  
 F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:35//CAENORHAB  
 DITIS ELEGANS.//P20630  
 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-31:102:67  
 //HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04174  
 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//HOMO  
 SAPIENS (HUMAN).//P51805  
 F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILLOMAVIR  
 US TYPE 5.//P06924  
 F-NT2RP2001601  
 F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:59:32/  
 /GALLUS GALLUS (CHICKEN).//P19601  
 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:140:33  
 //SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P35220  
 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC RE  
 GION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40358  
 F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO  
 -LYASE) (NON- NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//1.2e-2  
 6:126:56//HOMO SAPIENS (HUMAN).//P06733  
 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5' REGION (ORF1).//

0.25:148:25//CAMPYLOBACTER JEJUNI.//Q46089  
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164  
 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-18:83:61//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2001699//PROTEIN C14.//0.98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21045  
 F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//Q99317  
 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50534  
 F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURUS (BOVINE).//P20072  
 F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RP2001762  
 F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//047040  
 F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009  
 F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE).//Q61466  
 F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS SCROFA (PIG).//019084  
 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008  
 F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHE

EP).//Q10991

F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS (HUMAN).//P32019

F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53946

F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:27//CANDIDA ALBICANS (YEAST).//P46593

F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273

F-NT2RP2001936

F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305

F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3' REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485

F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880

F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353

F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331

F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSERADISH TREE) (MORINGA PTERYGOSPERMA).//P24303

F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2002041

F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-NT2RP2002047

F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220

F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157

F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958

F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916

F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVIS ARIES (SHEEP).//Q02958

F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990

F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839

F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206

F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//HOMO SAPIENS (HUMAN).//P18146

F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM).//P01526

F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)

(IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)  
 (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDI  
 NG LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110  
 F-NT2RP2002172  
 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYC  
 ES CEREVISIAE (BAKER'S YEAST).//P48510  
 F-NT2RP2002192  
 F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGA  
 NS.//P34804  
 F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011  
 :45:40//HOMO SAPIENS (HUMAN).//060683  
 F-NT2RP2002219  
 F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)  
 )- TRANSLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43  
 436  
 F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP  
 34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37  
 318  
 F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTE  
 R).//P11414  
 F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLI  
 ZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84  
 //MUS MUSCULUS (MOUSE).//055127  
 F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAP  
 IENS (HUMAN).//P12524  
 F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REG  
 ION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930  
 F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABI

ES VIRUS (STRAIN KAPLAN) (PRV).//P24827

F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DI GLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLY CEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903

F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40 269

F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A ).//2.2e-06:145:26//CANDIDA BOIDINII (YEAST).//Q00316

F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REG ION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524

F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE). //P17599

F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:66:28//MINK CE LL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388

F-NT2RP2002394

F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:107:37// BOS TAURUS (BOVINE).//P02453

F-NT2RP2002426

F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32/ /PLASMODIUM BERGHEI (STRAIN ANKA).//P23093

F-NT2RP2002442//HESA PROTEIN.//6.0e-16:163:30//PLECTONEMA BORYANUM.//P46 037

F-NT2RP2002457

F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I./ /9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO S APIENS (HUMAN).//P50238

F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSP  
ORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//075027

F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:  
45//PSEUDOMONAS AERUGINOSA.//P04139

F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//1.3e-31:124:59//HOMO  
SAPIENS (HUMAN).//Q02386

F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155)  
(155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT).  
//P37199

F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.94:83:28  
//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680

F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4  
.0e-10:194:23//CAENORHABDITIS ELEGANS.//Q11073

F-NT2RP2002546

F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGME  
NT).//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010

F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e  
-19:60:61//HOMO SAPIENS (HUMAN).//P51523

F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (  
AFRICAN CLAWED FROG).//Q92125

F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:31//SACCHARO  
MYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REG  
ION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264

F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//6.  
2e-37:180:44//RATTUS NORVEGICUS (RAT).//Q63009

F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA  
GMENT).//0.98:37:35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879

F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP

34.5).//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37  
319

F-NT2RP2002672//PROTEIN Q300.//0.0018:41:43//MUS MUSCULUS (MOUSE).//Q027  
22

F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3  
.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180.//0.00027:139:33//PSEUDORA  
BIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//6.9e-09:96:40//MUS MUSCULUS  
(MOUSE).//P55194

F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//3.6e-20  
:160:36//RATTUS NORVEGICUS (RAT).//P49816

F-NT2RP2002736

F-NT2RP2002740

F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2.//2.0e-07:178:28//SACCHA  
ROMYCES CEREVISIAE (BAKER'S YEAST).//P51862

F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72  
//HOMO SAPIENS (HUMAN).//P39191

F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T.//0.95:33:39//YERSI  
NIA PSEUDOTUBERCULOSIS.//Q00932

F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA  
-GLUCANASE) (CELLULASE).//0.71:78:33//TRICHODERMA LONGIBRACHIATUM.//Q127  
14

F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR.//0.44:76:32//STR  
ONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P11994

F-NT2RP2002778

F-NT2RP2002800//CRAMBIN.//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAM  
BE).//P01542

F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CON



TAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.010:87:31//HOMO SAPIENS (HUMAN)  
 .//P02812

F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.  
 00018:57:45//RATTUS NORVEGICUS (RAT).//P04474

F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION  
 .//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP2002880//DNA REPAIR PROTEIN RAD32.//0.83:67:28//SCHIZOSACCHAROMYC  
 ES POMBE (FISSION YEAST).//Q09683

F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT).//0.99:70:24//  
 RATTUS NORVEGICUS (RAT).//Q64204

F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (AL  
 PHA-1A ADRENERGIC RECEPTOR).//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100

F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCH  
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P40968

F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 D2013.2 IN CHROMOSOME II.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q189  
 64

F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHAT  
 E-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0022:98:39//CANIS FAM  
 ILIARIS (DOG).//P30803

F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.  
 0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43333

F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U  
 BIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//2.8  
 e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICU  
 S (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669

F-NT2RP2002979

F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.1e-09:98:36//MYCOPLASMA CA  
 PRICOLUM.//P10129

F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN).//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//054888

F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-19:62:64//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44204

F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0051:16:87//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP2003099

F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIENS (HUMAN).//P04281

F-NT2RP2003117

F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572

F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303

F-NT2RP2003129

F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117

F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217

F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//043242

F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP2003164//ZYXIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523

F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-24:77:64/  
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III./  
/2.3e-14:87:37//CAENORHABDITIS ELEGANS.//P30629

F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.  
0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P4  
1306

F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P  
1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991

F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDY  
LCHOLINE TRANSFER PROTEIN) (PI/PC TP).//1.0:51:31//CANDIDA GLABRATA (YEA  
ST) (TORULOPSIS GLABRATA).//P53989

F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.1e-44:66:84/  
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOC  
OCCUS PYOGENES.//P02977

F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P4150  
5

F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (F  
RAGMENT).//5.5e-06:78:35//BRASSICA NAPUS (RAPE).//P40603

F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (U  
P-FRAMESHIFT SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (B  
AKER'S YEAST).//P30771

F-NT2RP2003280

F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-P  
HOSPHATE CYCLASE) (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISI

AE (BAKER'S YEAST).//Q08096  
 F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:175:33//HOMO SAPIENS (HUMAN).//P51522  
 F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO SAPIENS (HUMAN).//P23246  
 F-NT2RP2003297  
 F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT).//P37285  
 F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886  
 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//CAENORHABDITIS ELEGANS.//P34284  
 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P01416  
 F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//061570  
 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01408  
 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189  
 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//0.94:29:34//ARAUCARIA HETEROPHYLLA.//P37843  
 F-NT2RP2003394  
 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P45746  
 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS NORVEGICUS (RAT).//P38378  
 F-NT2RP2003445

F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENO  
VIRUS TYPE 2.//P03290

F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MA  
RCHANTIA POLYMORPHA (LIVERWORT).//P12168

F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESAT  
URASE).//6.7e-06:108:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2)  
(T-14-6).//7.2e-15:38:50//GALLUS GALLUS (CHICKEN).//Q98937

F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q6  
3003

F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0  
e-11:91:43//SUS SCROFA (PIG).//P04175

F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25/  
/DROSOPHILA MELANOGASTER (FRUIT FLY).//P35416

F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HO  
MO SAPIENS (HUMAN).//P23246

F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYC  
OBACTERIUM TUBERCULOSIS.//Q10696

F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS  
TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19283

F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HO  
MO SAPIENS (HUMAN).//P08547

F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (R  
AT).//P09951

F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E).//0.98:37:37//HOMO SAPIENS (HUM  
AN).//Q14657

F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//6.4e-35:175:44//HOMO SAPIENS (HUMAN).//P19474

F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X.//0

.72:82:34//CAENORHABDITIS ELEGANS.//Q22544  
 F-NT2RP2003581//HOMEBOX PROTEIN OTX1.//0.90:61:37//MUS MUSCULUS (MOUSE)  
 .//P80205  
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P).//0.83:61:32//MYCOPLASMA GENI  
 TALIIUM.//P47272  
 F-NT2RP2003604//ALPHA-CATENIN.//1.5e-11:152:33//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P35220  
 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE  
 2-ACYLHYDROLASE).//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK  
 RATTLESNAKE).//P00623  
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-  
 N- ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC  
 ACID SYNTHETASE).//3.9e-12:84:40//NEISSERIA MENINGITIDIS.//Q57385  
 F-NT2RP2003668//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.0e-33:74:81/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.7e-05:40:67//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.5e-37:56:67/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5' REGION (EC 1.-.-.-  
 ) (ORFA).//1.3e-07:98:37//LISTERIA MONOCYTOGENES.//P25145  
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (G  
 AMMA- GLUTAMYLTRANSFERASE 5) (GGT-REL).//0.66:23:52//HOMO SAPIENS (HUMAN  
 ).//P36269  
 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTID  
 ASE A) (APA) (DIFFERENTIATION ANTIGEN GP160).//1.2e-22:187:35//HOMO SAPI  
 ENS (HUMAN).//Q07075  
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (U  
 BIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DE

UBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2).//2.7e-06:119:34//HOMO S  
 APIENS (HUMAN).//P35125  
 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
 ).//6.7e-27:68:75//HOMO SAPIENS (HUMAN).//Q05481  
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG.//0.64:110:30//MYCOPL  
 ASMA PNEUMONIAE.//P75105  
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U  
 BIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.2  
 e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGIC  
 US (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669  
 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR.//0.67:68:30//PSEUDOTERRA  
 NOVA DECIPIENS (COD WORM).//P26914  
 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
 //1.0e-98:235:82//BOS TAURUS (BOVINE).//P53620  
 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.011:69:34//ORGY  
 IA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341  
 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:33:36//  
 EQUUS CABALLUS (HORSE).//P48663  
 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAG  
 MENT).//0.029:35:42//PSEUDOMONAS AERUGINOSA.//P23621  
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION./  
 /0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA).//P14728  
 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//4.  
 7e-54:204:47//CAENORHABDITIS ELEGANS.//Q09201  
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN).//0.61:30:36//HEVEA BRASIL  
 ENSIS (PARA RUBBER TREE).//P80359  
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//1.0:35:37//CA  
 NIS FAMILIARIS (DOG).//P13206  
 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//2

.5e-05:80:38//CAENORHABDITIS ELEGANS.//Q11076  
 F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.54:28:50/  
 /ESCHERICHIA COLI.//P05834  
 F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P36193  
 F-NT2RP2003871  
 F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:  
 28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736  
 F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-  
 RELATED PROTEIN KINASE 1).//4.8e-110:268:80//MUS MUSCULUS (MOUSE).//P519  
 54  
 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)  
 (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:9  
 2:31//RATTUS NORVEGICUS (RAT).//009175  
 F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.  
 2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-21:62:62//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-  
 08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702  
 F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P3  
 7806  
 F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.3e-19:47:70/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.2e-18:80:58/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTIO  
 N FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290  
 F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CI



NC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746  
 F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).  
 //P17599  
 F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP).//Q26181  
 F-NT2RP2004066//CALDESMON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN).//P12957  
 F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187  
 F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404  
 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:31//GALLUS GALLUS (CHICKEN).//P02314  
 F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262  
 F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09010  
 F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS MUSCULUS (MOUSE).//P05143  
 F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051  
 F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (HUMAN).//Q15697  
 F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730  
 F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS E

DULIS (BLUE MUSSEL).//P80247  
 F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//  
 0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737  
 F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLY  
 CEPHALUM (SLIME MOLD).//P90587  
 F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-  
 48:211:51//HOMO SAPIENS (HUMAN).//Q15139  
 F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.  
 //0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489  
 F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN  
 ) (MT-CE).//1.0:39:28//CAENORHABDITIS ELEGANS.//P17512  
 F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN  
 RGP1).//0.0036:64:28//ORYZA SATIVA (RICE).//P25766  
 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:21:42//  
 PONGO PYGMAEUS PYGMAEUS (BORNEAN ORANGUTAN).//P92896  
 F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.0002  
 3:118:33//NEPHILA CLAVIPES (ORB SPIDER).//P46804  
 F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAVIRUS T  
 YPE 8.//P06425  
 F-NT2RP2004316  
 F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//SYNECH  
 OCYSTIS SP. (STRAIN PCC 6803).//Q01904  
 F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.0e-33:84:77/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II.  
 //0.78:96:30//CAENORHABDITIS ELEGANS.//Q09556  
 F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN  
 VP9).//0.059:143:30//BOVINE ROTAVIRUS (STRAIN UK).//P04515  
 F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT).//0.27:38:39//EIMERIA ACER

VULINA.//P21959

F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR.//0.64:71:28//MAREK'S DISEASE H  
ERPEVIRUS (STRAIN GA) (MDHV).//P52510

F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE  
RICH GLYCOPROTEIN) (HPRG) (FRAGMENT).//0.59:50:40//ORYCTOLAGUS CUNICULU  
S (RABBIT).//Q28640

F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III./  
/4.0e-16:89:43//CAENORHABDITIS ELEGANS.//P34388

F-NT2RP2004392

F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN.//0.42:89:2  
9//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10080

F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE).//1.0:72:34//MES  
OCRICETUS AURATUS (GOLDEN HAMSTER).//P37886

F-NT2RP2004400

F-NT2RP2004412//SPERM PROTAMINE P1.//0.24:38:31//NOTORYCTES TYPHLOPS (MA  
RSUPIAL MOLE).//P42143

F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40.//0.0087:197:22//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (AL  
PHA-2AAR).//1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338

F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT  
(RBE-II).//0.20:68:36//RATTUS NORVEGICUS (RAT).//Q07652

F-NT2RP2004490//FOS-RELATED ANTIGEN 1.//0.94:59:33//HOMO SAPIENS (HUMAN)  
.//P15407

F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRA  
GMENTS).//1.0:37:32//PISASTER OCHRACEUS (SEA STAR).//P24998

F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-15:57:71/  
/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPT

IC VESICLES).//1.2e-48:121:60//HOMO SAPIENS (HUMAN).//Q12756  
 F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65).//1.0:20:50//EUGLEN  
 A GRACILIS.//P32095  
 F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//5.2e-07:  
 150:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09903  
 F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.7e-37:100:78  
 //HOMO SAPIENS (HUMAN).//P39192  
 F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC R  
 EGION.//8.2e-06:150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321  
 4  
 F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II.//  
 0.84:105:24//CAENORHABDITIS ELEGANS.//Q09458  
 F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS)./  
 /0.17:127:29//RATTUS NORVEGICUS (RAT).//P30009  
 F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:50:58//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS  
 (STRAIN COPENHAGEN).//P20561  
 F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42//ARAB  
 IDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250  
 F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I  
 .//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10328  
 F-NT2RP2004675  
 F-NT2RP2004681  
 F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REG  
 ION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243  
 F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS  
 JANNASCHII.//Q58063  
 F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (F

SSION YEAST).//P41891

F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-15:97:49//

HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPH

ILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICO

N ESCULENTUM (TOMATO).//Q00451

F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RIC

H KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./

/P38692

F-NT2RP2004775

F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T

RNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996

F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR

(EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:

133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3' REGION.//0.018:86

:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-NT2RP2004816//H58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40

336

F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P707

42

F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:

39//OVIS ARIES (SHEEP).//P02443

F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA G

LAUCA (SWAMP OAK).//Q39511

F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINA

SE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355

F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).

//0.87:36:33//ECTOTHIORHODOSPIRA VACUOLATA.//P38524  
 F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTO  
 R) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220  
 F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIA  
 A0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q0673  
 0  
 F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.17:28:57//HO  
 MO SAPIENS (HUMAN).//P39189  
 F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS  
 TENAX. VIRUS 1 (STRAIN KRA1) (TTV1).//P19301  
 F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE  
 SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002  
 F-NT2RP2004982  
 F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAP  
 IENS (HUMAN).//Q14157  
 F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:  
 26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378  
 F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SA  
 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965  
 F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.9  
 0:54:31//HOMO SAPIENS (HUMAN).//P22531  
 F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e  
 -30:78:56//MUS MUSCULUS (MOUSE).//P15533  
 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMY  
 CES CEREVISIAE (BAKER'S YEAST).//P14906  
 F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTE  
 INS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED V  
 IRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P06937  
 F-NT2RP2005020

F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:10  
6:35//PODOSPORA ANSERINA.//Q00808

F-NT2RP2005031

F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32447

F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL AD  
DITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFER  
ASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//057486

F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS ELEGANS.  
//P17656

F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPH  
A SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P3446  
6

F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:  
46:39//PLEUROCHYSIS HAPTONEMOFERA.//P41552

F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//B  
OS TAURUS (BOVINE).//P25508

F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARD  
IA THETA (CRYPTOMONAS PHI).//078517

F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P5  
0586

F-NT2RP2005147

F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//  
0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (S  
PINACH).//P12164

F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG  
ION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.8  
e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839

F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//3.9  
e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624

F-NT2RP2005227

F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALB  
ICANS (YEAST).//P87185

F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48  
//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970

F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS  
GALLUS (CHICKEN).//P17277

F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-C  
HAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS  
(RAT).//035547

F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAG  
MENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031

F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI.//1.0:42:28//RHIZOBIUM LEGUMINO  
SARUM (BIOVAR VICIAE).//P28151

F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70/  
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICO  
BACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972

F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDI  
TIS ELEGANS.//P18832

F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROT  
EIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAP  
IENS (HUMAN).//P10645

F-NT2RP2005336//HYPOTHETICAL 68.7 KD.PROTEIN IN STB1-MCK1 INTERGENIC REG  
ION.//0.00011:124:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42846

F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38).//4  
.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12675



F-NT2RP2005354

F-NT2RP2005358//MYOSIN IC HEAVY CHAIN.//0.012:91:39//ACANTHAMOEBA CASTEL  
LANII (AMOEBA).//P10569

F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10).//0.0022:73:36//ORYCTOL  
AGUS CUNICULUS (RABBIT).//P48038

F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.  
00085:135:28//CAENORHABDITIS ELEGANS.//Q09202

F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDAS  
E) (SE).//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32476

F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0011:  
54:42//ZEA MAYS (MAIZE).//P14918

F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.039:182:29//MUS  
MUSCULUS (MOUSE).//P05142

F-NT2RP2005453

F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.  
3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//4.0e-10:124:37//BOS TA  
URUS (BOVINE).//Q02827

F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN.//0.96:42:33//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P20553

F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//4.6e-09:92:42//SACC  
HAROMYCES CEREVISIAE (BAKER'S YEAST).//P38127

F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129.//0.76:80:32//BORRELIA BURGD  
ORFERI (LYME DISEASE SPIROCHETE).//051155

F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-31:39:89/  
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2005490//METALLOTHIONEIN-II (MT-II).//0.14:27:33//SCYLLA SERRATA  
(MUD CRAB).//P02806

F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6).//0.9  
5:45:31//METHANOCOCCUS JANNASCHII.//Q58785

F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION.//0.99:68:30//BACTERIOPHAGE T4.//Q02407

F-NT2RP2005496//ZINC FINGER PROTEIN 135.//1.4e-54:120:59//HOMO SAPIENS (HUMAN).//P52742

F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA A ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//9.5e-76:146:86//RATTUS NORVEGICUS (RAT).//P36876

F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP).//0.025:70:40//HOMO SAPIENS (HUMAN).//P17931

F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:166:27//GALLUS GALLUS (CHICKEN).//P02457

F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//7.9e-45:118:79//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11.//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//051354

F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG).//9.8e-13:84:45//HOMO SAPIENS (HUMAN).//P29074

F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN).//4.9e-10:90:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ.//0.36:119:21//BACILLUS SUBTILIS.//P39115

F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III.//6.0e-39:179:46//CAENORHABDITIS ELEGANS.//Q09253

F-NT2RP2005555

F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I.//4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09790

F-NT2RP2005581

F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.014:37:40//HOMO SAPIENS (HUMAN).//P02811

F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247

F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950

F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN).//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54.//0.63:41:31//BRASSICA NAPUS (RAPE).//P43402

F-NT2RP2005645

F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).//0.0023:50:42//HOMO SAPIENS (HUMAN).//Q01860

F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RP2005669//METALLOTHIONEIN-II (MT-II).//0.76:16:50//SCYLLA SERRATA (MUD CRAB).//P02806

F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1).//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P49119

F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275.//0.17:50:40//HAEMOPHILUS INFLUENZAE.//P43975

F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708

F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAPIENS (HUMAN).//P02811

IENS (HUMAN).//Q15034  
 F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: P  
 EPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161  
 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II).//0.19:14:50//STENELLA COERUL  
 EOALBA (STRIPED DOLPHIN).//P14425  
 F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTO  
 LAGUS CUNICULUS (RABBIT).//P02456  
 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//  
 HOMO SAPIENS (HUMAN).//P16415  
 F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HO  
 MO SAPIENS (HUMAN).//P39192  
 F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALL  
 IDUM.//083390  
 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA  
 ROBUSTA (FRUIT FLY).//Q03296  
 F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTU  
 S NORVEGICUS (RAT).//P13432  
 F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO  
 SAPIENS. (HUMAN).//P17034  
 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//  
 HOMO SAPIENS (HUMAN).//P02461  
 F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:  
 37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181  
 F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCH  
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P11633  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P  
 5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322

F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYZOLAGUS CUNICULUS (RABBIT).//P42675

F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P08393

F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:43:55//OWENIA FUSIFORMIS.//P21260

F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004

F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//O07401

F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34223

F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:28:53//HOMO SAPIENS (HUMAN).//P22532

F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.99:33:48//BACTERIOPHAGE T4.//P22917

F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT I I).//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853

F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:28/

/TETRAHYMENA THERMOPHILA.//P40631

F-NT2RP2005890

F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:44/

/DROSOPHILA YAKUBA (FRUIT FLY).//P03933

F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65/

/HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:49//

ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347

F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
DENYLYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500

F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC RE  
GION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185

F-NT2RP2006023//DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N) (FRAGM  
ENT).//1.0:40:45//VIBRIO CHOLERAEE.//P52118

F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III./  
/4.0e-11:90:34//CAENORHABDITIS ELEGANS.//P34281

F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (F  
RAGMENT).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636

F-NT2RP2006052//METALLOTHIONEIN-I (MT-I).//0.19:31:38//CERCOPITHECUS AET  
HIOPS (GREEN MONKEY) (GRIVET).//P02797

F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTU  
S NORVEGICUS (RAT).//P02466

F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//042184

F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REG  
ION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651

F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:34//OPHIO  
PHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P80156

F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP  
. (STRAIN PCC 6803).//P73014

F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS ELEGANS.  
//P08124

F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1  
.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2006166

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REG  
ION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917

F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUS  
CULUS (MOUSE).//P20357

F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-05:49:61/  
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//  
HOMO SAPIENS (HUMAN).//P05997

F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOG  
ASTER (FRUIT FLY).//P22468

F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEI  
N).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141

F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//M  
US MUSCULUS (MOUSE).//P05143

F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS  
TYPE 1 (RHPV 1).//P24834

F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANN  
AMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058

F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.  
2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROT  
EIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625

F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGME  
NT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV

-1).//P04612

F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0051:25:76//  
HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HO  
MO SAPIENS (HUMAN).//P42768

F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALU  
S DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333

F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURS  
OR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41  
//TRICHOMONAS VAGINALIS.//P53401

F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.  
3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842

F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66/  
/CONUS MAGUS (MAGUS CONE).//P37300

F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOME  
BOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658

F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUT  
TATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238

F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS  
ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-NT2RP2006456

F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT  
VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN  
PCC 7002) (AGMENELLUM QUADRUPLICATUM).//P31087

F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORH  
ABDITIS ELEGANS.//Q21184

F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCH  
ANTIA POLYMORPHA (LIVERWORT).//P12202

F-NT2RP2006534



F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//032723

F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603

F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP1B10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791

F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BOVINE).//P02318

F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296

F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755

F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755

F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695

F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-17:64:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-CO  
A CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//  
P49787

F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHA  
ROMYCES CEREVISIAE (BAKER'S YEAST).//P40986

F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLA  
SMA GENITALIUM.//P47529

F-NT2RP3000134

F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE  
(FISSION YEAST).//P41891

F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:3  
6//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694

F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.3e-15:36:83//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.91:21:  
52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL  
PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SA  
CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
.//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808

F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLI  
FERA (HONEYBEE).//P15858

F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAP  
IENS (HUMAN).//Q93075

F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLO  
ID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5' REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103

F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253

F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (0182).//0.38:77:33//ESCHERICHIA COLI.//P09160

F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//067825

F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097

F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482

F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP3000348

F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5' REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103

F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:84//BOS TAURUS (BOVINE).//P08760

F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19735

F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293

F-NT2RP3000393//HOMEBOX PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:36:52//  
HOMO SAPIENS (HUMAN).//P09017

F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX  
PROTEIN 13).//5.5e-27:116:44//MUS MUSCULUS (MOUSE).//035286

F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCH  
AROMYCES CEREVISIAE (BAKER'S YEAST).//P33203

F-NT2RP3000418//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.2e-16:228:34//MUS MUSCULUS  
(MOUSE).//P11369

F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGI  
ON.//9.8e-10:201:26//ESCHERICHIA COLI.//P37908

F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.91:48:3  
5//MYCOBACTERIUM LEPRAE.//P38388

F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:3  
3//GALLUS GALLUS (CHICKEN).//P23681

F-NT2RP3000451

F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00018:178:36//  
RATTUS NORVEGICUS (RAT).//P02454

F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)  
(GIF).//0.098:40:27//BOS TAURUS (BOVINE).//P37359

F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16  
:81//VOLVOX CARTERI.//P21997

F-NT2RP3000512

F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACT  
ERIOPHAGE LAMBDA.//P03769

F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e  
-16:234:30//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:  
192:30//HOMO SAPIENS (HUMAN).//P15151

F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGME  
NT).//0.60:51:39//ASTERINA PECTINIFERA (STARFISH).//P11958

F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//ME  
THANOCOCCUS JANNASCHII.//Q57866

F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)  
.//0.99:26:34//DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULAN  
S (FRUIT FLY).//O18666

F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC R  
EGION.//1.5e-26:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3875  
5

F-NT2RP3000582

F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (M  
OUSE).//P02798

F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P332  
88

F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIEN  
S (HUMAN).//O00268

F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGAST  
ER (FRUIT FLY).//P25992

F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.  
00095:90:37//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RP3000603//5E5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//  
Q63003

F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (S  
TEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34  
//HOMO SAPIENS (HUMAN).//P36956

F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02\_ORF427).//0.15  
:52:36//MYCOPLASMA PNEUMONIAE.//P75277

F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//Q93073

F-NT2RP3000628

F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967

F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.7e-40:102:79  
//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II.  
//6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441

F-NT2RP3000665//HOMEODOMAIN PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//075360

F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5' REGION (ORFY).//0.26:202:23//CLOSTRIDIUM KLUYVERI.//P38943

F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P00817

F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516

F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10688

F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q06852

F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS

S (CHICKEN).//P26990  
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:37//PS  
 EUDOMONAS DENITRIFICANS.//P00103  
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.  
 22)).//0.82:51:39//MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458  
 F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.025:79:37//B  
 OS TAURUS (BOVINE).//P25508  
 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT  
 ).//0.85:36:47//MYCOPLASMA CAPRICOLUM.//P43040  
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (E  
 C 2.4.1.17) (UDPGT) (UGT1\*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGME  
 NT).//1.0:70:34//MUS MUSCULUS (MOUSE).//Q62452  
 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-  
 ).//5.2e-72:247:61//HOMO SAPIENS (HUMAN).//P27448  
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIEN  
 S (HUMAN).//P50876  
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-31:90:75/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCINE MAX  
 (SOYBEAN).//P24337  
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SA  
 IMIRI (STRAIN 11).//Q01042  
 F-NT2RP3000865  
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//  
 1.4e-09:232:28//GALLUS GALLUS (CHICKEN).//P29616  
 F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGA  
 NS.//P17656  
 F-NT2RP3000875//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2).  
 //0.90:62:37//MUS MUSCULUS (MOUSE).//P43241

F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.99:124:33//BOS TAURUS (BOVINE).//P02453

F-NT2RP3000904

F-NT2RP3000917//DHP1 PROTEIN.//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P40848

F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//2.4e-19:159:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P39027

F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN).//0.24:19:47//ESCHERIC HIA COLI.//P13946

F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//1.4e-10:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159

F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X.//0.70:50:32//CAENORHABDITIS ELEGANS.//Q11084

F-NT2RP3001007

F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG.//1.3e-05:138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P36416

F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744).//4.0e-28:141:51//HOMO SAPIENS (HUMAN).//Q02386

F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//3.8e-08:144:29//CAENORHABDITIS ELEGANS.//P34568

F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//3.4e-06:217:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65.//1.1e-30:244:33//RATTUS NORVEGICUS (RAT).//Q64375

F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT).//0.041:47:44//HOMO SAPIENS (HUMAN).//P54793

F-NT2RP3001109



F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.17:28:39//DROSOP  
HILA MELANOGASTER (FRUIT FLY).//Q01644

F-NT2RP3001113//INVOLUCRIN.//0.00036:192:23//MUS MUSCULUS (MOUSE).//P489  
97

F-NT2RP3001115

F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT).//0.99:29:51//  
STREPTOMYCES LIVIDANS.//Q54340

F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).//0.0015:73:39//BO  
S TAURUS (BOVINE).//Q29442

F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.3e-57:229:52//  
HOMO SAPIENS (HUMAN).//P16415

F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC RE  
GION.//2.8e-07:83:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888

F-NT2RP3001133//CALCIUM BINDING PROTEIN.//2.0e-08:171:32//DICTYOSTELIUM  
DISCOIDEUM (SLIME MOLD).//P35085

F-NT2RP3001140//F-SPONDIN PRECURSOR.//2.0e-147:244:97//RATTUS NORVEGICUS  
(RAT).//P35446

F-NT2RP3001147//TROPOMYOSIN 2 (TMII).//0.11:159:23//SCHISTOSOMA MANSONI  
(BLOOD FLUKE).//P42638

F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2.//6.2e-09:163:25//MUS MUSC  
ULUS (MOUSE).//Q06666

F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN)  
(CHROMOSOME REPLICATION PROTEIN CHL15).//4.1e-05:244:23//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//Q01454

F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIA  
LOPHORIN) (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3).//0.21:13  
6:26//MUS MUSCULUS (MOUSE).//P15702

F-NT2RP3001214//SAP1 PROTEIN.//0.058:133:30//SACCHAROMYCES CEREVISIAE (B  
AKER'S YEAST).//P39955

F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//2.1  
e-08:137:33//HOMO SAPIENS (HUMAN).//P35663

F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.  
11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS SP  
. (STRAIN AK-1).//P80193

F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3' REGION (FRAGMENT  
).//0.75:57:31//ESCHERICHIA COLI.//P33792

F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN MUSCULOAP  
ONEUROTIC FIBROSARCOMA VIRUS AS42.//P23091

F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.  
2e-55:221:49//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400

F-NT2RP3001245

F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I)./  
/0.0042:142:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491

F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89:43//HOM  
O SAPIENS (HUMAN).//P53420

F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194:44//HOMO  
SAPIENS (HUMAN).//Q02386

F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I./  
/8.2e-17:183:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199

F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP  
5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.7e-09:78:39//MUS MUSCULU  
S (MOUSE).//Q60676

F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.7e-08:38:71//  
HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159:70/  
/HOMO SAPIENS (HUMAN).//Q92556

F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46:39//ORNITHORHYNCHUS ANATINU  
S (DUCKBILL PLATYPUS).//P35307

F-NT2RP3001318

F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73:24//BRACHYDANIO  
RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98874

F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAG  
MENT).//0.0021:56:35//HOMO SAPIENS (HUMAN).//P17037

F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90:33//MUS MUSCULUS (MOUSE).//P  
49025

F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202:34//HUMAN CYTOME  
GALOVIRUS (STRAIN AD169).//P16818

F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRAN  
SPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129:33//  
HOMO SAPIENS (HUMAN).//P53007

F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66:28//DIC  
TYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RP3001374

F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//H  
OMO SAPIENS (HUMAN).//P23246

F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS  
(FRUIT FLY).//P13424

F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22:45//C  
APRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834

F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//STRAWBER  
RY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV).//Q00848

F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (F  
RAGMENT).//1.9e-08:45:37//HOMO SAPIENS (HUMAN).//P10073

F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P53538

F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P53009

F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS  
(STRAIN COPENHAGEN).//P20542

F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P  
43735

F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS  
(HUMAN).//Q14191

F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN)  
.//P12270

F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA  
GMENT).//0.96:52:21//TARSUS SYRICHTA (TARSIER).//Q36151

F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION  
(ORF1).//0.96:45:35//ESCHERICHIA COLI.//P14505

F-NT2RP3001449//HOMEODOMAIN PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.0043:53:4  
3//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:40//DROS  
OPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55  
:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767

F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMOEBA CASTEL  
LANII (AMOEBA).//P10569

F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:43//SACCH  
AROMYCES CEREVISIAE (BAKER'S YEAST).//P11632

F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA  
NAPUS (RAPE).//P43402

F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:14  
8:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940

F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.13:44:38//BO  
S TAURUS (BOVINE).//P25508

F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS V

IRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA IN TERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641

F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN IN CWH-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772

F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820

F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362

F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:177:25//ZEA MAYS (MAIZE).//P14918

F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG).//P80236

F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//Q92609

F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:34//ORGANIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3001672

F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS.//P26843

F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//1.5e-07:63:44//CAENORHABDITIS ELEGANS.//P34679

F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI).//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065

F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:24//HOMO SAPIENS (HUMAN).//P12883

F-NT2RP3001698

F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54356

F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618

F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HOMO SAPIENS (HUMAN).//O14646

F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//CAENORHABDITIS ELEGANS.//P34669

F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//Q14141

F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+)/DICARBOXYLATE COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545

F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-21:60:85/  
/HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPI  
ENS (HUMAN).//Q14140

F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC  
3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36  
//HOMO SAPIENS (HUMAN).//Q16828

F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.  
-).//0.0096:204:25//CANDIDA ALBICANS (YEAST).//Q92212

F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44/  
/PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694

F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.  
8e-33:159:53//HOMO SAPIENS (HUMAN).//P52272

F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (E  
HS-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOT  
HIORHODOSPIRA HALOCHLORIS.//P80103

F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//  
HOMO SAPIENS (HUMAN).//P08123

F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (  
FRAGMENT).//0.99:43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466

F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEI  
N).//9.3e-10:213:24//STREPTOCOCCUS PYOGENES.//P30141

F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//2.6e  
-61:220:60//HOMO SAPIENS (HUMAN).//P55347

F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:21  
3:24//PODOSPORA ANSERINA.//Q00808

F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.  
074:124:34//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLO

MAVIRUS (COPV).//Q89420  
 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021  
 :237:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12114  
 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC R  
 EGION.//1.0:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880  
 F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-14:35:60/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC RE  
 GION.//0.86:162:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040  
 F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (ST  
 RAIN RICE) (PRV).//P07645  
 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//  
 1.0:113:27//ESCHERICHIA COLI.//P23839  
 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.  
 //4.1e-56:208:47//CAENORHABDITIS ELEGANS.//Q09251  
 F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIARA CO  
 PROPHILA (FUNGUS GNAT).//P22312  
 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0:41:31  
 //MUS MUSCULUS (MOUSE).//P02319  
 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.2e-44:69:79/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.000  
 24:45:40//MUS MUSCULUS (MOUSE).//Q61345  
 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEU  
 RONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACEL  
 LULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPI  
 ENS (HUMAN).//P24821  
 F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./  
 /1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232



F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//000198

F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP HA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (MOUSE).//P17427

F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.046:176:31//STREPTOMYCES FRADIAE.//P20186

F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NORVEGICUS (RAT).//P41777

F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577

F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094

F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INFLUENZAE.//P43709

F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986

F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-17:37:75//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//

0.011:166:28//HOMO SAPIENS (HUMAN).//P10163  
 F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING  
 PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170  
 F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA  
 FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.028:191:29//HOMO SAPIENS  
 (HUMAN).//000268  
 F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:9  
 1//MUS MUSCULUS (MOUSE).//Q02614  
 F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLU  
 S CASEI.//P55153  
 F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.4e-26:114:62  
 //HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01645  
 F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:  
 62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102  
 F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIB  
 RIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080  
 F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//M  
 US MUSCULUS (MOUSE).//P05143  
 F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P45978  
 F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS T  
 YPE 16.//P06922  
 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//  
 1.7e-42:191:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014171  
 F-NT2RP3002304  
 F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P561

F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q  
63003

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (E  
C 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOC  
HONDRIAL PRECURSOR.//1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995

F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 1  
02) (NEUROENDOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//  
Q92796

F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCE  
S CEREVISIAE (BAKER'S YEAST).//P53327

F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//S  
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53091

F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:36  
//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM T  
UMEFACIENS.//P50018

F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I./  
/0.00032:52:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438

F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REG  
ION.//9.4e-42:209:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007

F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REG  
ION.//7.7e-32:162:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059

F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G  
11.03C.//2.1e-45:241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09  
805

F-NT2RP3002545

F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III./  
/2.8e-41:161:52//CAENORHABDITIS ELEGANS.//Q10010

F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIE

S VIRUS (STRAIN KAPLAN) (PRV).//P33479  
 F-NT2RP3002587  
 F-NT2RP3002590  
 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)  
 (THIOREDOXIN- RELATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES C  
 EREVISIAE (BAKER'S YEAST).//P17967  
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3' REGION.//1.0:65:4  
 0//STREPTOMYCES CACAOI.//P33654  
 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTI  
 S SP. (STRAIN PCC 6803).//P50027  
 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (  
 HUMAN).//P07438  
 F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q9083  
 0  
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:33/  
 /HOMO SAPIENS (HUMAN).//P08123  
 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS  
 ELEGANS.//P37165  
 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS  
 (HUMAN).//P22059  
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SK01-RPL44A INTERGENIC  
 REGION.//6.0e-38:203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P538  
 93  
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .25:63:31//ARTEMIA SALINA (BRINE SHRIMP).//P19049  
 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REG  
 ION.//0.029:60:36//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (AC  
 MNPV).//P41469  
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULU

S (MOUSE).//Q60575  
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:109:33//MUS MUSCULUS (MOUSE).//P15265  
 F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).//0.77:70:32//HOMO SAPIENS (HUMAN).//Q13206  
 F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-11:66:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014056  
 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS MUSCULUS (MOUSE).//Q05722  
 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371  
 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0034:35:65//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790  
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II).//0.97:23:39//BRYONIA DIOICA (RED BRYONY).//P11968  
 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00017:140:31//RATTUS NORVEGICUS (RAT).//P04474  
 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP).//4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625  
 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217

F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450

F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445

F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//060488

F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566

F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553

F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESA (PLAICE).//P07216

F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705

F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879

F-NT2RP3003032

F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254

F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157

F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//033780

F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552

F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT)./  
/0.028:165:31//VULPES VULPES (RED FOX).//P53353

F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0  
e-14:243:25//ESCHERICHIA COLI.//P02981

F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALL  
US GALLUS (CHICKEN).//P46936

F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULU  
S (MOUSE).//P33174

F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZ  
OSACCHAROMYCES POMBE (FISSION YEAST).//Q92337

F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG)  
(BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (  
HUMAN).//Q08431

F-NT2RP3003150

F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e  
-79:260:54//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (F  
ISSION YEAST).//Q02088

F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (  
HUMAN).//P52742

F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REG  
ION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966

F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//  
9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCO  
IDEUM (SLIME MOLD).//P32252

F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENI

C REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3819  
0  
F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES C  
EREVISIAE (BAKER'S YEAST).//P32583  
F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (B  
OVINE).//Q92176  
F-NT2RP3003242//STANNIOCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (HUMAN).//P52823  
F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533  
F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920  
F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344  
F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054  
F-NT2RP3003290//BIOH PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001  
F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.2 1.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//064948  
F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547  
F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//ACANTHA MOEBA CASTELLANII (AMOEBA).//P05659  
F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162  
F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191  
F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681



F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991

F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.9e-26:74:78  
//HOMO SAPIENS (HUMAN).//P39191

F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III./  
/3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641

F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP3003384

F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q60649

F-NT2RP3003403

F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//O15370

F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2.//P11300

F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:41//HOLOTRICHIA DIOMPHALIA.//Q25055

F-NT2RP3003433

F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3003490

F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PROTEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472

F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HOMO SAPIENS (HUMAN).//P29400

F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURUS

S (BOVINE).//P20072

F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529

F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TURKIP YELLOW MOSAIC VIRUS.//P10358

F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:32//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS (DOG).//P24409

F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).//2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748

F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIORERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90267

F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755

F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060

F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209

F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601

F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P02314

F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVEGICUS (RAT).//P35446

F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014

F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN.//0.47:109:28//AGROBACTERIUM TUMEFACIENS.//P05680

F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3' REGION (ORF1).//0.57:34:38//AZORHIZOBIUM CAULINODANS.//P26486

F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR.//0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//P78744

F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).//4.2e-51:72:95//GALLUS GALLUS (CHICKEN).//P00523

F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION.//0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36121

F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.028:135:35//GALLUS GALLUS (CHICKEN).//P12105

F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT).//0.0026:90:33//HORDEUM VULGARE (BARLEY).//P06472

F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//5.6e-20:174:31//BOS TAURUS (BOVINE).//P02720

F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0017:111:38//CANIS FAMILIARIS (DOG).//P30803

F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).//1.1e-37:187:42//MUS MUSCULUS (MOUSE).//P008600

F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION.//1.0:38:39//ESCHERICHIA COLI.//P75979

F-NT2RP3003842

F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB).//0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125

F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943

F-NT2RP3003932

F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:32//THERMOTOGA MARITIMA.//P35874

F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67).//0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476

F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS NORVEGICUS (RAT).//P51400

F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.00021:64:40//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P41479

F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE).//0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153

F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-11:51:72//

HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS  
 (MOUSE).//P48379  
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REG  
 ION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757  
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:72:65//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-10:51:72/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (H  
 UMAN).//P51815  
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS SO  
 BRIA.//P09165  
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (D  
 OMESTIC PIGEON).//P15786  
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:1  
 78:89//RATTUS NORVEGICUS (RAT).//Q63619  
 F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:21  
 5:24//PODOSPORA ANSERINA.//Q00808  
 F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA MELAN  
 OGASTER (FRUIT FLY).//P17886  
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:33//CAENORHABDI  
 TIS ELEGANS.//P20630  
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC<sup>s</sup> 3.1.2.15) (U  
 BIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DE  
 UBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:  
 207:29//HOMO SAPIENS (HUMAN).//Q13107  
 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:3  
 1//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179

F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.  
 //1.1e-64:191:63//CAENORHABDITIS ELEGANS.//P34657

F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (H  
 UMAN).//P25440

F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//1.1e-07:184:35//  
 BOS TAURUS (BOVINE).//P02453

F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40.//4.9e-08:98:39//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (  
 HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT)  
 .//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073

F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTE  
 R).//P11414

F-NT2RP3004334

F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX).//0.91:110:26//MUS MUSCULUS  
 (MOUSE).//P46660

F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.  
 //0.60:198:24//CAENORHABDITIS ELEGANS.//P46012

F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76/  
 /HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGI  
 ON (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854

F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMUL  
 ATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS  
 (HUMAN).//Q92674

F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q1  
 3155

F-NT2RP3004428//METALLOTHIONEIN-A (MTA).//0.0010:36:47//STRONGYLOCENTROT  
US PURPURATUS (PURPLE SEA URCHIN).//P04734

F-NT2RP3004451//MYOSIN IC HEAVY CHAIN.//0.00072:113:34//ACANTHAMOEBA CAS  
TELLANII (AMOEBA).//P10569

F-NT2RP3004454//VERPROLIN.//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BA  
KER'S YEAST).//P37370

F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215.//0.0013:125:32//HUMAN ADENOV  
IRUS TYPE 2.//P03291

F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III  
.//1.0:33:51//CAENORHABDITIS ELEGANS.//Q09254

F-NT2RP3004472//GERM CELL-LESS PROTEIN.//7.3e-33:170:40//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//Q01820

F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//8.4  
e-54:214:46//HOMO SAPIENS (HUMAN).//P98171

F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.9e  
-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110

F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.  
0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REG  
ION PRECURSOR.//0.066:87:35//BACILLUS SUBTILIS.//P50840

F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69  
//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40.//0.64:93:34//SACCHAROMYCES CER  
EVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//2.2e-16:90:42//SACCHAROMY  
CES CEREVISIAE (BAKER'S YEAST).//P40484

F-NT2RP3004527

F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6.//0.38:148:22//SACCHAROMYCES CERE  
VISIAE (BAKER'S YEAST).//P32943

F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1).//0.38:89:38//RATTUS NORVEGICUS (RAT).//P21743

F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2).//0.0024:200:24//MYCOPLASMA PNEUMONIAE.//P75471

F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT).//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18713

F-NT2RP3004569//ANKYRIN.//8.3e-07:150:28//MUS MUSCULUS (MOUSE).//Q02357

F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325

F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q02224

F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTOCOCCUS FAECIUM).//P13692

F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//4.5e-08:149:30//CAENORHABDITIS ELEGANS.//P34681

F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.0e-24:75:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54352

F-NT2RP3004670//CUTICLE COLLAGEN 2.//0.00090:159:29//CAENORHABDITIS ELEGANS.//P17656

F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79:243:62//BOS TAURUS (BOVINE).//P35526

F-NT2RP4000023

F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALLUS GALLUS (CHICKEN).//



P12957

F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GALLUS (CHICKEN).//Q9083  
0

F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-24:182:31//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP4000102//XPAR7 PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q991  
66

F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//P24014

F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q  
10568

F-NT2RP4000129//5E5 ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//  
Q63003

F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P35197

F-NT2RP4000150

F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//  
4.2e-31:180:47//CAENORHABDITIS ELEGANS.//P32740

F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM DIS  
COIDEUM (SLIME MOLD).//P14328

F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC RE  
GION.//2.4e-08:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEI  
N).//5.4e-05:143:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P2828  
4

F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:35//SACCH  
AROMYCES CEREVISIAE (BAKER'S YEAST).//P22579

F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20

:104:40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287  
 F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203  
 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q90830  
 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:207:76//MUS MUSCULUS (MOUSE).//Q03173  
 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:43//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//023968  
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS (BOVINE).//P20072  
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5e-71:209:66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115  
 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404  
 F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370  
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531  
 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC REGION.//0.75:125:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596  
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.27:92:33//RATTUS NORVEGICUS (RAT).//P10164  
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN ADENOVIRUS TYPE 41.//P23691  
 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:163:52//HOMO SAPIENS (HUMAN).//075570

F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:12  
5:80//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR  
OTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246

F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOM  
O SAPIENS (HUMAN).//Q99676

F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC RE  
GION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST  
) .//P47179

F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2  
-MANNOSIDASE 1B).//1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098

F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-15:72:61/  
/HOMO SAPIENS (HUMAN).//P39195.

F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-23:63:82/  
/HOMO SAPIENS (HUMAN).//P39192

F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)  
.//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294

F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:  
30//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (U  
BIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DE  
UBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROT  
EASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009

F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULA  
TORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276

F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-0  
5:152:23//CAENORHABDITIS ELEGANS.//Q09475

F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROM  
YCES CEREVISIAE (BAKER'S YEAST).//P40484

F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III./  
/1.3e-23:165:35//CAENORHABDITIS ELEGANS.//P34535

F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NU  
CLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).  
//P15396

F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA F  
ABA (BROAD BEAN).//Q41657

F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAR  
OMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BO  
S TAURUS (BOVINE).//P25508

F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0  
.37:187:24//STREPTOCOCCUS AGALACTIAE.//P27951

F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P33755

F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS  
GALLUS (CHICKEN).//P13544

F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III./  
/4.3e-14:174:34//CAENORHABDITIS ELEGANS.//Q03574

F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III./  
/2.1e-19:155:36//CAENORHABDITIS ELEGANS.//P34679

F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIR  
US TYPE 2.//P03290

F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR  
SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188  
:44//GALLUS GALLUS (CHICKEN).//P30352

F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:  
40:40//GLYCINE MAX (SOYBEAN).//Q05544

F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-06:31:74//

HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP4000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOC  
 CUS JANNASCHII.//Q58465  
 F-NT2RP4000704  
 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e  
 -07:134:40//STREPTOMYCES FRADIAE.//P20186  
 F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TR  
 ANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//1.1e-62:109:88//HOMO SAPIENS  
 (HUMAN).//P10266  
 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:2  
 5//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//H  
 OMO SAPIENS (HUMAN).//P23246  
 F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//  
 ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655  
 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE  
 GION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915  
 F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//HELIANTHUS  
 ANNUUS (COMMON SUNFLOWER).//P29675  
 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32583  
 F-NT2RP4000833  
 F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.18:38:44//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAF  
 II-90).//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38129  
 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)  
 (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:2  
 29:53//RATTUS NORVEGICUS (RAT).//009175

F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//  
HOMO SAPIENS (HUMAN).//P16415

F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCUL  
US (MOUSE).//035682

F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:  
268:43//HOMO SAPIENS (HUMAN).//P22314

F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.  
112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B).//5.4e-10:220:25//HOMO  
SAPIENS (HUMAN).//Q16620

F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60/  
/ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:3  
2//BACILLUS SUBTILIS.//P39217

F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROT  
EIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828

F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN)  
(IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)./  
/P29128

F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DI  
GLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLY  
CEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG  
SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903

F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC  
REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288

F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6.//2.0e-05:102:37//CAEN  
ORHABDITIS ELEGANS.//P34391

F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REG  
ION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P

EPITIDE P-D] (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIR  
 US (STRAIN COPENHAGEN).//P20517  
 F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.  
 //0.90:94:25//CAENORHABDITIS ELEGANS.//P34343  
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XA  
 NTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531  
 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02  
 722  
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7  
 .7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUB  
 UNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//054888  
 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSI  
 S THALIANA (MOUSE-EAR CRESS).//Q42377  
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REG  
 ION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840  
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL  
 PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640  
 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT  
 I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROS  
 OPHILA MELANOGASTER (FRUIT FLY).//P13002  
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T  
 RNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996  
 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III./  
 /0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664  
 F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q9083  
 0  
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TA

FII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//000268

F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586

F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099

F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911

F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563

F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736

F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793

F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896

F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750

F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:10



6:41//VOLVOX CARTERI.//P21997  
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331  
 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:17:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643  
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178  
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:17:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643  
 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307  
 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DERMORPHIN].//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422  
 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360  
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12404  
 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//P36787  
 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124  
 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA COLI.//P05834  
 F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273  
 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241

F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787

F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108:31//PODOSPORA ANSERINA.//Q00808

F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOC CUS JANNASCHII.//Q58220

F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III./1.4e-18:244:27//CAENORHABDITIS ELEGANS.//Q10123

F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN).//P53760

F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//5.7e-11:229:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//0.00088:84:28//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN).//0.51:92:26//ONCHOCERCA VOLVULUS.//P36991

F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160

F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION.//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767

F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER).//P38767

R).//P11414  
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//  
 HOMO SAPIENS (HUMAN).//Q02224  
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIE  
 NS (HUMAN).//Q14141  
 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216  
 :56//HOMO SAPIENS (HUMAN).//P28160  
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7  
 .6) (VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)./  
 /P18616  
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//A  
 RTEMLA SALINA (BRINE SHRIMP).//P02399  
 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CE  
 REVISIAE (BAKER'S YEAST).//P21560  
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC  
 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPI  
 ENS (HUMAN).//Q02218  
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2  
 .3e-24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC  
 REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40  
 206  
 F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELE  
 GANS.//P34804  
 F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS  
 LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (  
 SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561  
 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT  
 I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:79:41//DROSO

PHILA MELANOGASTER (FRUIT FLY).//P13002  
 F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENE  
 C REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25  
 656  
 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30//SACCH  
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P32558  
 F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:24  
 //MYCOBACTERIUM TUBERCULOSIS.//P96902  
 F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT)./  
 /0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170  
 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:4  
 2//HOMO SAPIENS (HUMAN).//Q15057  
 F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-  
 50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS T  
 AURUS (BOVINE).//P06836  
 F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
 //6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620  
 F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS  
 PYOGENES.//P16946  
 F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA  
 LIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803)./  
 /P73505  
 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//  
 SUS SCROFA (PIG).//P27917  
 F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO  
 SAPIENS (HUMAN).//P02811  
 F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT)  
 .//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462  
 F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//4.2e-21:2

49:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469  
 F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-1  
 8:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323  
 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II./  
 /3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600  
 F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43//MYCO  
 BACTERIUM TUBERCULOSIS.//Q10690  
 F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:103:72  
 //HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:37:37//C  
 HLORELLA VULGARIS.//P56338  
 F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//4.3e-1  
 1:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282  
 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR ( .  
 EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY)  
 .//Q09332  
 F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//1.0:6  
 7:34//HOMO SAPIENS (HUMAN).//P31260  
 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGM  
 ENT).//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506  
 F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28//HOMO  
 SAPIENS (HUMAN).//P11274  
 F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION  
 FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q07231  
 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENORHABDIT  
 IS ELEGANS.//P20630  
 F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAPIENS ( .  
 HUMAN).//O14817  
 F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:42//CAEN

ORHABDITIS ELEGANS.//P34391  
 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727  
 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO  
 SAPIENS (HUMAN).//Q13330  
 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:14  
 1:22//RATTUS NORVEGICUS (RAT).//P98089  
 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS  
 (MOUSE).//P55194  
 F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REG  
 ION.//0.92:39:51//BACILLUS SUBTILIS.//P55185  
 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VI  
 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDEN  
 T RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MU  
 SCULUS (MOUSE).//Q05921  
 F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 IN PMT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIA  
 E (BAKER'S YEAST).//P42935  
 F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTO  
 LAGUS CUNICULUS (RABBIT).//P48038  
 F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SA  
 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024  
 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS  
 (MOUSE).//P24399  
 F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77)  
 (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPART  
 YL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)  
 .//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209  
 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSC

ULUS (MOUSE).//P11260  
 F-NT2RP4001953  
 F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLU  
 S SUBTILIS.//Q07833  
 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RI  
 FTIA PACHYPTILA (TUBE WORM).//P30754  
 F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65/  
 /SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943  
 F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I./  
 /0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844  
 F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI  
 CASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875  
 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46/  
 /MYCOBACTERIUM TUBERCULOSIS.//Q10888  
 F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:  
 36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P1880  
 4  
 F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
 ).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481  
 F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACT  
 OR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670  
 F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29  
 :55//OWENIA FUSIFORMIS.//P21260  
 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZ  
 OSACCHAROMYCES POMBE (FISSION YEAST).//P38938  
 F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLO  
 RI (CAMPYLOBACTER PYLORI).//P56027

F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALL  
IDUM.//083371

F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGME  
NT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012

F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (M0-10).//0.027:40:40/  
/MUS MUSCULUS (MOUSE).//P02831

F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT  
) .//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779

F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:21  
5:28//PODOSPORA ANSERINA.//Q00808

F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL  
PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//S  
ACCHAROMYCES CEREVISIAE (BAKER' S YEAST).//P08640

F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MU  
S MUSCULUS (MOUSE).//P05142

F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//DROSOPH  
ILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (  
FRAGMENT).//0.92:49:32//PARACOCCLUS DENITRIFICANS.//P29969

F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7  
e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116

F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//  
RATTUS NORVEGICUS (RAT).//P02454

F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALO  
BACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331

F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q9  
9501

F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHARO  
MYCES CEREVISIAE (BAKER' S YEAST).//P19658



F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).  
//P02262

F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROM  
YCES POMBE (FISSION YEAST).//P87060

F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30/  
/GALLUS GALLUS (CHICKEN).//P02457

F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS  
ELEGANS.//P17657

F-OVARC1000035

F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM  
DISCOIDEUM (SLIME MOLD).//P34143

F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (R  
NASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022

F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSA  
MBICA (MOZAMBIQUE COBRA).//P01452

F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15  
) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).  
//P13662

F-OVARC1000085

F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS  
(RAT).//Q02874

F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCU  
LUS (MOUSE).//Q06666

F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHA  
MOEBA CASTELLANII (AMOEBE).//P46756

F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC R  
EGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935

F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (F  
RAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600

F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (ST  
RAIN KASZA) (SPV).//P32217

F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-28:57:63/  
/HOMO SAPIENS (HUMAN).//P39194

F-OVARC1000133

F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (U  
BIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DE  
UBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:  
200:29//HOMO SAPIENS (HUMAN).//Q13107

F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (Z  
EBRAFISH) (ZEBRA DANIO).//Q01702

F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12  
:175:29//CANDIDA ALBICANS (YEAST).//P46593

F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAP  
IENS (HUMAN).//P50876

F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0030:77:38//H  
OMO SAPIENS (HUMAN).//P39188

F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:35//ESC  
HERICHIA COLI.//P32056

F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268

F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REG  
ION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03677

F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS  
MUSCULUS (MOUSE).//P05142

F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-10:41:78/  
/HOMO SAPIENS (HUMAN).//P39193

F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-L  
IKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSC  
ULUS (MOUSE).//P97481

F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770

F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//P23249

F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBYA GOSSYPII (EREMOTHECIUM GOSSYPII).//Q00063

F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5.2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014179

F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPIENS (HUMAN).//P04281

F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004

F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CYANOPHORA PARADOXA.//P48273

F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:115:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05049

F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGICUS (RAT).//P28023

F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIIIC INTERGENIC REGION.//1.0:46:34//BACILLUS SUBTILIS.//P54431

F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067

F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION.//0.70:21:47//BACILLUS SUBTILIS.//P39150

F-OVARC1000431

F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q0420

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F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059

F-OVARC1000442

F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCHUS CONTORTUS.//P16252

F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIODAR TRIFOLII).//P42710

F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-08:29:93//HOMO SAPIENS (HUMAN).//P39192

F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8e-06:96:36//RATTUS NORVEGICUS (RAT).//Q63340

F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:48:37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//P31567

F-OVARC1000486

F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS JANNASCHII.//Q58610

F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:40//EIMERIA ACERVULINA.//P09125

F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02722

F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO SAPIENS (HUMAN).//Q16612

F-OVARC1000543//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.

41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTI  
DE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:35//HO  
MO SAPIENS (HUMAN).//Q10472  
F-OVARC1000556  
F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:80:47//  
HOMO SAPIENS (HUMAN).//P39188  
F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//  
0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2)./  
/P17760  
F-OVARC1000573  
F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVIN  
E).//P46159  
F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).//0.023:96:36//BO  
S TAURUS (BOVINE).//P02459  
F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOM  
O SAPIENS (HUMAN).//P09001  
F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME)  
(GLE).//0.91:134:28//CHLAMYDOMONAS REINHARDTII.//P31178  
F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.6e-36:100:80  
//HOMO SAPIENS (HUMAN).//P39189  
F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//  
ODONTELLA SINENSIS.//P49535  
F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.00  
36:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357  
F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATT  
US NORVEGICUS (RAT).//P02466  
F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//  
ESCHERICHIA COLI.//P05834  
F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TR

ANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//E  
 SCHERICHIA COLI.//P08374

F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722

F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2  
 -MANNOSIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098

F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POM  
 ATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS  
 NORVEGICUS (RAT).//P02684

F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO  
 SAPIENS (HUMAN).//P02811

F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUC  
 OSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHAS  
 E A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70/  
 /BOS TAURUS (BOVINE).//P08037

F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III./  
 /5.2e-29:224:36//CAENORHABDITIS ELEGANS.//Q18262

F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPH  
 ILA MELANOGASTER (FRUIT FLY).//P25159

F-OVARC1000769

F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS  
 (HUMAN), AND CANIS FAMILIARIS (DOG).//P08886

F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC  
 HOMEBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS S  
 CROFA (PIG).//Q29303

F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-31:47:82/  
 /HOMO SAPIENS (HUMAN).//P39189

F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.

16:55:40//CAENORHABDITIS ELEGANS.//Q10926  
 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//P35465  
 F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P08199  
 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION.//6.9e-09:180:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991  
 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52490  
 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484  
 F-OVARC1000883//METALLOTHIONEIN-1.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15113  
 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440  
 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.00033:60:45//BOS TAURUS (BOVINE).//P02465  
 F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774  
 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//P15606  
 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10337  
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELEGANS.//Q09455  
 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HUMAN).//P56524

F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA  
 CONSTRICTOR (BOA).//P92848

F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGI  
 ON.//1.0:48:33//ESCHERICHIA COLI.//P45505

F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOM  
 O SAPIENS (HUMAN).//P02452

F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS  
 TYPE 1 (MAV-1).//P12533

F-OVARC1000948

F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS  
 JANNASCHII.//Q58343

F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-32:56:75/  
 /HOMO SAPIENS (HUMAN).//P39193

F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGRE  
 GATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOS  
 AE (EASTERN JAMESON' S MAMBA).//P28375

F-OVARC1000971

F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC  
 REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER' S YEAST)  
 .//P53832

F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06  
 138

F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROT  
 EIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264

F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:43:90/  
 /HOMO SAPIENS (HUMAN).//P39195

F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01642

F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS



JANNASCHII.//Q58336

F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949

F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).//Q05561

F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640

F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338

F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194

F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637

F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490

F-OVARC1001062

F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44951

F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//O69162

F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291

F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I./

/0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197  
 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC RE  
 GION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079  
 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSAC  
 CHAROMYCES POMBE (FISSION YEAST).//P78963  
 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANO  
 GA (FRUIT FLY).//P48608  
 F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).  
 //P11339  
 F-OVARC1001118  
 F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS  
 .//066439  
 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MU  
 SCULUS (MOUSE).//P28798  
 F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:8  
 7:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177  
 F-OVARC1001162  
 F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070  
 F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,  
 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS  
 MUSCULUS (MOUSE).//P97323  
 F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUM  
 AN).//P02814  
 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00023:28:75//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-OVARC1001173  
 F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BAR  
 R VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMY

CES CEREVISIAE (BAKER'S YEAST).//P48510  
 F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P5321  
 5  
 F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057  
 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOC  
 CUS JANNASCHII.//Q58633  
 F-OVARC1001240  
 F-OVARC1001243  
 F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN).//P25440  
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//Q06666  
 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:41//PSEUDOMONAS AERUGINOSA.//P24563  
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281  
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504  
 F-OVARC1001282  
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968  
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013695  
 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTP T).//1.3e-14:150:28//ZEA MAYS (MAIZE).//P49133  
 F-OVARC1001330

F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02926

F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-OVARC1001342

F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//STAPHYLOCOCCUS CARNOSUS.//P36253

F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05890

F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634

F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS TAURUS (BOVINE).//P02465

F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13).//Q47100

F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SULF-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039

F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162

F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.062:18:77//HOMO SAPIENS (HUMAN).//P39195

F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570

F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//Q05482

F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO S

APIENS (HUMAN).//Q03692  
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30  
 //TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283  
 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDEL  
 LA TRISERIALIS (LEECH).//P17138  
 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)  
 (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184  
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P53290  
 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//M  
 US MUSCULUS (MOUSE).//Q02788  
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS IN  
 FLUENZAE.//P44149  
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAP  
 IENS (HUMAN).//P56545  
 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDN  
 EY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161  
 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//  
 1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077  
 F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOM  
 O SAPIENS (HUMAN).//P35325  
 F-OVARC1001547  
 F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCE  
 S CEREVISIAE (BAKER'S YEAST).//P53081  
 F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR  
 SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:  
 81//GALLUS GALLUS (CHICKEN).//P30352  
 F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2  
 B.//P15898

F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (S  
N-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:3  
9//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898

F-OVARC1001611

F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//O  
.30:43:34//CAENORHABDITIS ELEGANS.//Q11116

F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0e-19:45:82/  
/HOMO SAPIENS (HUMAN).//P39192

F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//O  
60248

F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE  
NUCLEOTIDE- BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1  
).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514

F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1  
B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267

F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATE  
D DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVI  
NE).//P07106

F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMY  
LASE INHIBITOR OF MICROBES I).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS  
(STREPTOMYCES CORCHORUSII).//P09921

F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:8  
7//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173

F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A  
2 B.//P15902

F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERM  
INAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P12945

F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS

ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911

F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//0.99:113:27//ESCHERICHIA COLI.//P23839

F-OVARC1001768

F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945

F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878

F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTEURYS TRISTIS (SPIDER).//P36984

F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796

F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RAT TUS NORVEGICUS (RAT).//P02454

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260

F-OVARC1001828

F-OVARC1001846

F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216

F-OVARC1001873

F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//CAENORHABDITIS ELEGANS.//Q09296

F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812

F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408

F-OVARC1001901

F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P34789

F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174

F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050

F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945

F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664

F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360

F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS (MOUSE).//P02319

F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1002044



F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3  
.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939

F-OVARC1002066

F-OVARC1002082

F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.99:149:  
24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS  
(RAT).//Q02874

F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MEL  
ANOGASTER (FRUIT FLY).//P50887

F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG  
6).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328

F-OVARC1002143

F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE  
GION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGI  
ON.//8.2e-07:119:35//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:  
45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204

F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN  
D2013.2 IN CHROMOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q189  
64

F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.  
//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725

F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q0272  
2

F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3  
(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING P

ROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547

F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474

F-PLACE1000031

F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-12:97:41//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-125).//P38373

F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258

F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046

F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538

F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HUMAN).//Q92934

F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS (MOUSE).//P06798

F-PLACE1000094

F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290

F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084

F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924

F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637

F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-AL

PHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640  
 F-PLACE1000214  
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GA  
 LLUS GALLUS (CHICKEN).//P02457  
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE  
 HERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUB  
 TYPE 2).//Q00039  
 F-PLACE1000292  
 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:4  
 2//MEDICAGO SATIVA (ALFALFA).//P11728  
 F-PLACE1000332  
 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALL  
 IDUM.//083435  
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C)  
 .//1.0:63:25//ORYCTOLAGUS CUNICULUS (RABBIT).//P16973  
 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (  
 PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CER  
 EVISIAE (BAKER'S YEAST).//P36027  
 F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q1  
 3496  
 F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN).//0.00023:145:30//MUS M  
 USCULUS (MOUSE).//P54320  
 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:9  
 0:63//HOMO SAPIENS (HUMAN).//Q15233  
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-  
 OXO-DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368  
 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//  
 0.48:72:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080

F-PLACE1000424

F-PLACE1000435

F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-31:129:63  
//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q0272  
2

F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO  
SAPIENS (HUMAN).//P08547

F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P807  
23

F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP  
-MANNOSE-1- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE  
).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS J  
ANNASCHII.//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37/  
/HOMO SAPIENS (HUMAN).//P15803

F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e  
-45:192:47//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE  
NUCLEOTIDE- BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//  
P32455

F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DRO  
SOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN  
ADENOVIRUS TYPE 12.//P36707

F-PLACE1000610

F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC R

EGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558  
 F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS TH  
 ALIANA (MOUSE-EAR CRESS).//Q08891  
 F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (A  
 CETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)./  
 /1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687  
 F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOP  
 ROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPR  
 ESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS  
 (HUMAN).//Q13263  
 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.//0.  
 93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934  
 F-PLACE1000716  
 F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3' REGION (ORF-11)./  
 /0.90:53:37//SHIGELLA FLEXNERI.//P55794  
 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA G  
 ENITALIUM.//P47394  
 F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-1  
 5:98:48//CAENORHABDITIS ELEGANS.//P34529  
 F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021  
 F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45//MYCO  
 BACTERIUM TUBERCULOSIS.//006360  
 F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.  
 //2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657  
 F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:12  
 8:30//HOMO SAPIENS (HUMAN).//P50552  
 F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//  
 HOMO SAPIENS (HUMAN).//P39188

F-PLACE1000841

F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY).//P23241

F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS JANNASCHII.//Q60319

F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899

F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRKII (YEAST) (HANSENULA MRKII).//P10410

F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO SAPIENS (HUMAN).//P49771

F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34109

F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941

F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097

F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796

F-PLACE1001000

F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584

F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P00987

F-PLACE1001015

F-PLACE1001024

F-PLACE1001036

F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA DIOMPHALIA.//Q25055

F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999

F-PLACE1001076

F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50//MEDICAGO SATIVA (ALFALFA).//P11728

F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.00063:125:32//CAENORHABDITIS ELEGANS.//Q11102

F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309

F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050

F-PLACE1001168

F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895

F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-PLACE1001238

F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087

F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040

F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAM

BICA (MOZAMBIQUE COBRA).//P01470  
 F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481  
 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636  
 F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620  
 F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:66:66//HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE1001323  
 F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/RS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971  
 F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12).//0.070:18:33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA).//P01422  
 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).//P17495  
 F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYOGENES.//P16947  
 F-PLACE1001384  
 F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929  
 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917  
 F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-32:47:74//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36/



/HOMO SAPIENS (HUMAN).//P04921  
 F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35/  
 /ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852  
 F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814  
 F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).//P11184  
 F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS JANNASCHII.//Q58019  
 F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480  
 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206  
 F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561  
 F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P21924  
 F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//048408  
 F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795  
 F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMORPHA (LIVERWORT).//P12196  
 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431  
 F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//Q60809  
 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164

F-PLACE1001608

F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896

F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640

F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523

F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//019926

F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.0:27:66//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842

F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635

F-PLACE1001705

F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME I.//6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013798

F-PLACE1001720

F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143

F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839

F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:90:56//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS  
(HUMAN).//Q14138

F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGU  
STIFOLIUS (NARROW-LEAVED BLUE LUPINE).//P09930

F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38  
//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042908

F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//9.2e-43:126:77  
//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYL  
ORI (CAMPYLOBACTER PYLORI).//P56057

F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:  
40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48994

F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REG  
ION.//9.5e-41:194:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262

F-PLACE1001799

F-PLACE1001810

F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR  
(EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:  
115:61//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

F-PLACE1001821

F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIE  
NS (HUMAN).//P01600

F-PLACE1001845

F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P53583

F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MI  
STLETOE).//P01540

F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKES  
SI (STOKES'S SEA SNAKE) (DSTEIRA STOKESI).//P01381

F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75  
:29//BACTERIOPHAGE NF.//P09877

F-PLACE1001928

F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABI  
ES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELL  
A CATARRHALIS.//Q49091

F-PLACE1002004

F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE  
)//Q61211

F-PLACE1002052

F-PLACE1002066

F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16  
:77:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.  
//4.0e-11:174:28//CAENORHABDITIS ELEGANS.//Q09564

F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e  
-57:112:99//HOMO SAPIENS (HUMAN).//076094

F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A)  
(MTCP-1 TYPE A) (P8MTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908

F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1)  
(IMMEDIATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULU  
S (MOUSE).//P17950

F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3' REGION (ORF 4).//  
0.0086:39:46//THIOBACILLUS FERROOXIDANS.//P20088

F-PLACE1002150

F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.4e-34:56:82/  
/HOMO SAPIENS (HUMAN).//P39189

F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BAR

K SCORPION).//P01492

F-PLACE1002170

F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591

F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738

F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5' REGION.//0.41:49:36//RHIZOBIUM LEGUMINOSARUM.//P14310

F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890

F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508

F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219

F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677

F-PLACE1002399

F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023

F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233

F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)

./Q04545

F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:1  
59:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013765

F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MO  
USE).//Q61555

F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HO  
MO SAPIENS (HUMAN).//P39193

F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULA  
TTA (RHESUS MACAQUE).//Q95196

F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2  
.9e-11:67:35//CAENORHABDITIS ELEGANS.//Q11096

F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFL  
UX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGI  
ON (071).//1.0:15:60//ESCHERICHIA COLI.//P46878

F-PLACE1002529

F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (M  
OUSE).//P70396

F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELA  
NOGASTER (FRUIT FLY).//P45890

F-PLACE1002578

F-PLACE1002583

F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BO  
VINE).//Q92176

F-PLACE1002598

F-PLACE1002604

F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//Q60604

F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086

F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//P38479

F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//Q62839

F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749

F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378

F-PLACE1002772

F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007

F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630

F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//MUS MUSCULUS (MOUSE).//Q60772

F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.46:35:42//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:201:74/  
/HOMO SAPIENS (HUMAN).//P56524

F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.6e  
-30:54:96//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS (MOUS  
E).//P02802

F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.77:35:37  
//VICIA ANGUSTIFOLIA (COMMON VETCH).//P01065

F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5' REGION (ORF1).//1.0:  
18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).  
//P36866

F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-27:91:70//  
HOMO SAPIENS (HUMAN).//P39188

F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III.  
//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548

F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-11:40:85/  
/HOMO SAPIENS (HUMAN).//P39195

F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:38:36//C  
ANIS FAMILIARIS (DOG).//P13206

F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.97:26:  
38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496

F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//METHANOC  
OCCUS JANNASCHII.//Q58560

F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REG  
ION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121

F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLON  
E 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012

F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P32583



F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME II  
I.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609  
F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P  
07791  
F-PLACE1003045  
F-PLACE1003092  
F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS  
(HUMAN).//Q13268  
F-PLACE1003108  
F-PLACE1003136  
F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS  
(BOVINE).//P18892  
F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA MIGRAT  
ORIA (MIGRATORY LOCUST).//Q01777  
F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBI  
QUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:  
38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743  
F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC RE  
GION.//0.24:74:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319  
F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P33750  
F-PLACE1003200  
F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSU  
S.//P42131  
F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:  
55//HOMO SAPIENS (HUMAN).//Q15391  
F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS  
(HUMAN).//Q14138  
F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER P

EPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522  
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAEN  
 ORHABDITIS ELEGANS.//P21541  
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SA  
 PIENS (HUMAN).//P11277  
 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e  
 -69:84:94//HOMO SAPIENS (HUMAN).//P51522  
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDI  
 NG PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083  
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2  
 B.//P15902  
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e  
 -05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378  
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:66:75/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIEN  
 S (HUMAN).//P35326  
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:  
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q0272  
 2  
 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS  
 MUSCULUS (MOUSE).//Q60890  
 F-PLACE1003383  
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORV  
 EGICUS (RAT).//P35287  
 F-PLACE1003401

F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37/  
/SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556  
F-PLACE1003454  
F-PLACE1003478  
F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//  
HOMO SAPIENS (HUMAN).//Q13201  
F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HO  
MO SAPIENS (HUMAN).//P08547  
F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.2e-17:77:50//  
HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIR  
US (ISOLATE HP-438 [MUNICH]).//P14366  
F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40/  
/XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931  
F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436  
F-PLACE1003553  
F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIR  
US (ISOLATE HP-438 [MUNICH]).//P14366  
F-PLACE1003575  
F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS T  
YPE 35.//P27226  
F-PLACE1003584  
F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998  
F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//  
OVIS ARIES (SHEEP).//078751  
F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-8  
7:238:67//CAENORHABDITIS ELEGANS.//P46975  
F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REG  
ION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554

F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHARO  
MYCES CEREVISIAE (BAKER'S YEAST).//Q02516

F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CAN  
IS FAMILIARIS (DOG).//P04542

F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEU  
S MIRABILIS.//P42275

F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q0272  
2

F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P227  
93

F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
NG FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170

F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REG  
ION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074

F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5  
.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724

F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0  
e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270

F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:1  
47:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRU  
CEI BRUCEI.//P00164

F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS  
DOMESTICA (APPLE) (MALUS SYLVESTRIS).//024058

F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//H  
OMO SAPIENS (HUMAN).//P08547

F-PLACE1003771

F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634

F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523

F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBIUS FORFICATUS.//Q02030

F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR.//0.0046:116:31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS).//052727

F-PLACE1003870

F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166:75//HOMO SAPIENS (HUMAN).//P51003

F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96:34//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.8e-54:260:46//BOS TAURUS (BOVINE).//P10895

F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792

F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS).//0.58:49:36//DAUCUS CAROTA (CARROT).//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYN

THETASE).//3.8e-52:92:85//HOMO SAPIENS (HUMAN).//P17812  
 F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05506  
 F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).//0.94:65:29//STREPTOCOCCUS EQUISIMILIS.//P30053  
 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074  
 F-PLACE1003936  
 F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385  
 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.9e-14:60:73//HOMO SAPIENS (HUMAN).//P39192  
 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102  
 F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-15:69:60//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//Q89420  
 F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387  
 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33485  
 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSIFORMIS.//P21260  
 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054  
 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817

F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//Q62556

F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COP ENHAGEN).//P21062

F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PI SUM SATIVUM (GARDEN PEA).//P13555

F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567

F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006

F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067

F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186

F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286

F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//P25508

F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB).//P37990

F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE).//Q62100

F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMYCES COELICOLOR.//P54741

F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12380

F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HUMAN).//P53420

F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33/

/GALLUS GALLUS (CHICKEN).//P02457  
 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//D  
 ROSOPHILA HYDEI (FRUIT FLY).//Q08696  
 F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.6e-28:46:76/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REG  
 ION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722  
 F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMI  
 NYLLACTOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (N  
 LBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HEL  
 ICOBACTER ACINONYX.//Q47947  
 F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.81:70:42//HO  
 MO SAPIENS (HUMAN).//P39195  
 F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:39//RA  
 TTUS NORVEGICUS (RAT).//Q63448  
 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD] , MITOCHONDRIAL SUBUNIT BE  
 TA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH  
 ) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE  
 ) (CYNOMOLGUS MONKEY).//Q28479  
 F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00013:40:62//  
 HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELAN  
 OGASTER (FRUIT FLY).//P25823  
 F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-10:33:87/  
 /HOMO SAPIENS (HUMAN).//P39193  
 F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e  
 -56:92:58//HOMO SAPIENS (HUMAN).//P51522  
 F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I./  
 /0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844



F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903  
 F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).  
 //0.58:66:34//HOMO SAPIENS (HUMAN).//P78358  
 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TA  
 FII-150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY)  
 .//Q24325  
 F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEIN  
 S (FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGA  
 L).//P14587  
 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS  
 EDULIS (BLUE MUSSEL).//P80248  
 F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIU  
 M CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P  
 19518  
 F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS  
 .//P17656  
 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
 SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q  
 10568  
 F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (H  
 UMAN).//Q13438  
 F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.  
 00036:100:30//PYROCOCCLUS FURIOSUS.//Q51731  
 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91  
 :58:29//KLEBSIELLA PNEUMONIAE.//Q48481  
 F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N  
 -METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32  
 //MUS MUSCULUS (MOUSE).//Q03391  
 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC RE

GION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781  
 F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//  
 7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704  
 F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)  
 .//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815  
 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MU  
 SCULUS (MOUSE).//Q60809  
 F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:48:62/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM./  
 /P55946  
 F-PLACE1004693  
 F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//  
 PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO).//Q35587  
 F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REG  
 ION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565  
 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//  
 RATTUS NORVEGICUS (RAT).//Q05175  
 F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.9e-09:37:70/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3' REGION.//0.99:72  
 :33//PSEUDOMONAS AERUGINOSA.//P21484  
 F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIA  
 LYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERA  
 SE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4  
 ).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206  
 F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./  
 /3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157  
 F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAE

RIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337  
 F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259  
 F-PLACE1004804  
 F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777  
 F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217  
 F-PLACE1004815  
 F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236  
 F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFORMIS.//P22754  
 F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072  
 F-PLACE1004838  
 F-PLACE1004840  
 F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891  
 F-PLACE1004885  
 F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499  
 F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042643  
 F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165  
 F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC R

EGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012  
 F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS  
 JANNASCHII.//Q57982  
 F-PLACE1004934  
 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (F  
 ISSION YEAST).//P87053  
 F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4  
 .0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073  
 F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (  
 BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478  
 F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.3e-30:55:72/  
 /HOMO SAPIENS (HUMAN).//P39192  
 F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:12  
 4:27//STREPTOCOCCUS PYOGENES.//P19401  
 F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//  
 LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942  
 F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOT  
 ES CRASSUS.//Q06183  
 F-PLACE1005027  
 F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAUR  
 US (BOVINE).//P20072  
 F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOP  
 HILA MELANOGASTER (FRUIT FLY).//Q01645  
 F-PLACE1005055  
 F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DRO  
 SOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-PLACE1005077  
 F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS

TUNETANUS (COMMON EUROPEAN SCORPION).//P55902  
 F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.5e-38:93:76/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100/  
 /HOMO SAPIENS (HUMAN).//P49753  
 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PRO  
 MOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38  
 //MUS MUSCULUS (MOUSE).//Q60821  
 F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR)  
 (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359  
 F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II  
 ).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608  
 F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (M  
 OUSE).//P47708  
 F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//  
 0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075  
 F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.0e-31:60:76/  
 /HOMO SAPIENS (HUMAN).//P39189  
 F-PLACE1005176  
 F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (ST  
 RAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831  
 F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHAS  
 E) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//N  
 EUROSPORA CRASSA.//P38678  
 F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRU  
 S (STRAIN COPENHAGEN).//P20511  
 F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIE  
 NS (HUMAN).//Q99218  
 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.00

17:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577  
 F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II./  
 /1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003  
 F-PLACE1005266  
 F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANO  
 GASTER (FRUIT FLY).//P42287  
 F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALL  
 US GALLUS (CHICKEN).//P53352  
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760  
 F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULG.  
 ARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020  
 F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGI  
 ON (O67).//0.15:36:41//ESCHERICHIA COLI.//P39355  
 F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)  
 .//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808  
 F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO  
 SAPIENS (HUMAN).//P11274  
 F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//M  
 US MUSCULUS (MOUSE).//P81067  
 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE  
 SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURI  
 DYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:28//SACCHAROMYCES CEREVI  
 SIAE (BAKER'S YEAST).//P48567  
 F-PLACE1005374  
 F-PLACE1005409  
 F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLU  
 CANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO)  
 .//P07979

F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOL  
 LANDIAE (SILVER GULL).//P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0  
 .23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSC  
 ULUS (MOUSE).//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HOR  
 DEUM VULGARE (BARLEY).//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFER  
 A (HONEYBEE).//P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DR  
 OSOPHILA MELANOGASTER (FRUIT FLY).//P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORA  
 BIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74/  
 /HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.  
 //9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III./  
 /3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPO  
 DOMYS CALIFORNICUS (KANGAROO RAT).//P16359

F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS  
 NEOFORMANS (FILOBASIDIELLA NEOFORMANS).//P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29/  
 /BOS TAURUS (BOVINE).//P03929

F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROS  
 OPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORA  
 BIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROT  
 EIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625

F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICU  
 M.//P30725

F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ER  
 K5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164

F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT  
 B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//  
 P40222

F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85)  
 (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894

F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIA  
 NA SYLVESTRIS (WOOD TOBACCO).//P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4  
 .1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (G  
 OLDEN HAMSTER).//Q60561

F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36:41//PORP  
 HYRA PURPUREA.//P51224

F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3' REGION (ORFC) (FRAGMENT).  
 //0.50:61:29//BACILLUS SUBTILIS.//P40405

F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (F  
 RAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603

F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCT  
 OLAGUS CUNICULUS (RABBIT).//P02456

F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53  
 //MUS MUSCULUS (MOUSE).//Q60710

F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REG



ION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
 F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E  
 C 3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT)./  
 /P08635  
 F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
 //0.028:96:32//HOMO SAPIENS (HUMAN).//P26371  
 F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (F  
 RUIT FLY).//P29617  
 F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.  
 //1.0:95:25//MUS MUSCULUS (MOUSE).//P17564  
 F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2  
 -MANNOSIDASE 1B).//2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098  
 F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REG  
 ION.//0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057  
 F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-23:56:76/  
 /HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIO  
 PHAGE 186.//P08711  
 F-PLACE1005845  
 F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.5e-28:96:73/  
 /HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1005851  
 F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
 SUBUNIT (CPSF 100 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q1  
 0568  
 F-PLACE1005884  
 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAR  
 OMYCES POMBE (FISSION YEAST).//P54069  
 F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3)

(EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//000483

F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURELIA.//P15617

F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01010

F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326

F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP).//0.64:57:33//RHODOFERAX FERMENTANS.//P80882

F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-PLACE1005966//TACHYPLESIN II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P14214

F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259

F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.5e-36:102:75//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473

F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+)) (ADP- RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q11207

F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOG).//Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:76//HOMO SAPIENS (HUMAN).//P56211

F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:40//ARACHIS HYPOGAEA (PEANUT).//P01066

F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//O00410

F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110

F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P1086

F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049

F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MOUSE).//P17427

F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864

F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965

F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-PLACE1006205

F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:22:50//MUS MUSCULUS (MOUSE).//P15265

F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805

F-PLACE1006236

F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS MUSCULUS (MOUSE).//Q61420

F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777

F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777

F-PLACE1006288

F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231

F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918

F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814

F-PLACE1006357

F-PLACE1006360

F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380

F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777

F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482

F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676

F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910

F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876

F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550

F-PLACE1006470

F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595

F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004

F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261

F-PLACE1006506

F-PLACE1006521

F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681

F-PLACE1006534

F-PLACE1006540

F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922

F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190

F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038

F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPLICATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861

F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529

F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//051371

F-PLACE1006640

F-PLACE1006673

F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1 ) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN] .//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295

F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENS).//Q59263

F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN). //1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198

F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941

F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517

F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875

F-PLACE1006792

F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972

F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569

F-PLACE1006805

F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102

F-PLACE1006860

F-PLACE1006867

F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3' REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087

F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281

F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567

F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1. PROTEIN.//0.95:86:26//USTILA GO MAYDIS (SMUT FUNGUS).//P22015

F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442

F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000

F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//000268

F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722

F-PLACE1006961

F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929

F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160

F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5' REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083

F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PR



OTEIN I2) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542  
F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//  
HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSC  
ULUS (MOUSE).//P11260  
F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0  
38:48:39//HOMO SAPIENS (HUMAN).//P22531  
F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL  
OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063  
F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGIO  
N.//0.97:47:29//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNP  
V).//P41663  
F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME I./  
/2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013730  
F-PLACE1007111  
F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA CO  
LI.//P03853  
F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//  
HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (F  
ISSION YEAST).//P41891  
F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCO  
BACTERIUM TUBERCULOSIS.//Q10826  
F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REG  
ION (O378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062  
F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//5.5e-10:  
98:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706  
F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELON  
GATION FACTOR A).//3.9e-19:96:57//HOMO SAPIENS (HUMAN).//P23193

F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).//1.0:132:30//RATTUS NORVEGICUS (RAT).//Q03386

F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981

F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608

F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//1.0:42:28//SUS SCROFA (PIG).//062697

F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200

F-PLACE1007286

F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749

F-PLACE1007317

F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318

F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715

F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561

F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).